

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTCCCTCAGCCCTGTAATTGGACATCTGCTGCTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG  
CTACCATTATGTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTAGGACTTCTATTGTCGAAACTT  
CCAGAAAACAACCCCTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTGGTATGGCTCAT  
TATATATGTTGTCAGACCATCCTTCTACCAAATGCAGCCAAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGGTTATCTGGTGTGGAGTAAGTCACCTAGCATGCTGACTTGCTC  
ATCAGTTTGACAGTGGCAATTGGGACTGATTTAGAACAGAAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGCTATGTCATTTCTTCTT  
GGTTTCTGACTTACATTGCTGATTTCAAGAAAATTCTTACGGGTGGAAGCCAATTAC  
TGGATTAACCCCTATGACACTGCACCTGCCCTATTAACAATGAACGAACACGGCTACTTCCA  
GAGATATTGATGAAAGGATAAAATTTCTGTAATGATTATGATTCTCAGGGATTGGGAAAGG  
TTCACAGAAGTTGCTTATTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAACACCTATGCCTATACCTTATCTCAGAAAATAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLHQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACGCGTGGCGGACCGTGGGGAGAGCCGCAGTCGGCTGCAGCACCTGGAGAAGGCAGACC  
GTGTAGGGGGCCTGTGGCCCCAGCGTGTGGCTGGGAGTGGAAAGTGGAGGCAGGAGCCTC  
CTTACACTTCGCCATGAGTTCTCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTG  
GATTTGGGTGGCTTCTTATGGCCAATTGTTAAAGACTATGAGATACTGAGTATGTTGACAG  
GTGATCTTCTCGTGTACGTTGCATTTCACCATGTTGAGCTCATCATCTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCGTTATTTCACTGGAAAATGAACCTGTGTAAATTGCTGATCTGG  
TTTCATGGTGCCTTACATGGCTATTGTTATTGAGCAATATCCGACTACTGCATAAACAGA  
CTGCTTTTCCTGTCTTATGGCTGACCTTATGTTATGTTCTGGAAACTAGGAGATCCCTTCC  
CATTCTCAGCCAAAACATGGATCTTATCCATAGAACAGCTCATGCCGGTTGGTGTGATTGGAG  
TGACTCTCATGGCTTCTTCTGGATTGGTGTCACTGCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATTCTAGCCCTGGAACGGGACTGCTGCAAACCATGGATATGAT  
CATAAAGAAAAAGAAAAGGATGGCAATGGCACGGAGAACATGTTCCAGAAGGGGAAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAAGTGTACCACTTCAGCATCAGGAAGTGAAGAAATCTTA  
CTTATTCAACAGGAAGTGGATGTTGGAGAATTAAGCAGGAGCTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTCAAGGGAAATATTTAATTCTGGTT  
ACTTTTCTTATTTACTGTGTTGGAAAATTTCATGGCTACCATCAATATTGTTTGATCGAGTT  
GGGAAAACGGATCTGTCAACAGAGGATTGAGATCACTGTGAATTATCTGGAAATCCAATTGATGT  
GAAGTTTGGTCCAACACATTCTCTCATCTGTGGAGAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTTACCAAGTTCTTATGCCATCTAGCAGTAAGTCTCCAATGTCATTGCTCTG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCTGTGCTGATCCGAATGAGTATGCCTT  
AGAATACCGCACCATATACTGAAGTCCTGGAGAACTGCAGTTCAACTTCTATCACCCTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTACGATACTCTCTCATTTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAATT  
GATATAAGAGGGGGAAAATGGAACCAGGGCTGACATTATAAACAAACAAATGCTATGGTAGC  
ATTTTACCTTCATAGCATACTCTTCCCCGTAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGAGAGAATCAACTCAAGACAATACTCAGCAGAGAGCATCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGGAGCCAAGAAACTAAAGGTGAAAATACACTGGAACCTGGCAAGACATGT  
CTATGGTAGCTGAGCCAACACGTAGGATTCCGTTAAGGTTCACATGGAAAGGTTAGCTT  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAAAGGGCGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCCATGGCCAACCTGTTATTGCAGCTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQLFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVDFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGD  
FPILSPKGILSIEQLISRVGIVGVTLMALLSGFGAVNCPTYMSYFLRNVTDIDILALERRLLQ  
TMDMIISKKKRMMARRTMFQKGEVHNKPSPFWGMIKSVTTSASGSENLTLIQQEVDALEELSRO  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQMIMGY  
FVSSVLLIRMSMPLERYRTIITEVLGELOQNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 5**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
AGAACTCTCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCACTGGCCATCTGAGGT  
GTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCAGGTGCTCAGGCTGGTGTGCTTCTCACT  
TCCATCTGGACCACGAGGCTCTGGTCCAAGGCTTTGCTGAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGATCACCCCTGTGAGCAAAAAGGCAACCCAGCAGCTGAATTTCACAG  
AAGCTAAGGAGGCCCTGTAGGCTGCTGGACTAACGTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGTGCTCATCTTAG  
GATTAGCCCAACCCCAAGTGTGGAAAAATGGGTGGGTCTGATTGGAAAGGTTCCAGTGA  
GCCGACAGTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACCTGTGATTCCAGAA  
ATTATCACCAACAAAGATCCCATTCAACACTCAAACCTGCAACACAAACAACAGAATTATTGT  
CACTGACAGTACCTACTCGGTGGCATCCCCACTCTACAATACCTGCCCTACTACTCCTC  
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAAATTGATTGTGTCACAGAAGTTTATG  
GAAACTAGCACCAGTCTACAGAAACTGAACCATTTGTGAAAATAAGCAGCATTCAAGAATGA  
AGCTGCTGGTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTCTCCCTTCTGGTCTG  
CAGCTGGCTTGGATTGCTATGTCAAAAGGTATGTCAAGGCCCTCCCTTACAACACAAGAAT  
CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA  
TGAGGAATCAAAGAAAATGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACACTACCGTGC  
GATGCCCTGGAAAGCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCCCTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAACAGTCCA  
CCCTGGTTCTTAACGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCAACAAAGAGAAT  
GCCCTCTCTTATTGTAACCCCTGTCTGGATCCTATCCTCTACCTCAAAGCTCCACGCCCT  
TTCTAGCCTGGCTATGCTTAATAATATCCCCTGGAGAAAGGAGTTTGCAAAGTGCAGGAC  
CTAAAACATCTCATCGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGACCCCTTCTCA  
GCTCTGAAAGAGAACACGTATCCACCTGACATGTCCTCTGAGGCCGTAAGAGCAAAGAAT  
GGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAGAAATAGAACACAGGCTGAGGATACGACAGTACACTGTCAGCAGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTGGAAACTCTGTTAGAACACACACA  
CTTACTTTCTGGTCTCTACCACTGCTGATATTCTCTGAGAAATATACTTTACAAGTAACA  
AAAATAAAAATCTTATAAAATTCTATTCTGAGTACAGAAATGATTACTAAGGAAGGATT  
ACTCAGTAATTGTTAAAAAGTAATAAAATTCAACAAACATTGCTGAATAGCTACTATATGTC  
AAAGTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCTCAAAAATTGCACATAGTAG  
AACGCTATCTGGGAAGCTATTTCAGTTGATATTCTAGCTTATCTACTTCAAACACTAAT  
TTTATTCTGAGACTAATCTTATTCAATTCTCTAATATGCCAACATTATAACCTTAATT  
TATTATAACACCTAACAGAAGTACATTGTTACCTATATACCAAGCACATTAAAGTGC  
ATTAACAAATGTATCACTAGCCCTCTTTCAACAAAGAAGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGVLIWKPVSQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTPPAPASTSIPR  
RKKLICVTEVMETSTMSTETEPFVENKAASKNEAAGFGGVPALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCCCGG  
GGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGAGCGAACCTCGTCCAGTCGGGGCG  
CGGCTGCGGGCGCAGAGCGGAGATCGAGCGGCTTGGGCCACCCCTGCTGTGCTGCTGGCG  
CGGCGGTCCCCACGGCCCCCGGCCGCTCCGACGGCACCTCGGCTCCAGTCAGCCCAGGGCG  
GCTCTCAGTACCCGAGGAGGCCACCCCTCAATGAGATGTTCCGAGGGTTGAGGAACGTGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGGGTGAAGAGATGGAGGCAGAAGAAGCTGCTGTA  
AAGCATCATCAGAAAGTGAACCTGGAAACTAACCTCCAGCTATACAATGAGACCAACACAGAC  
ACGAAGGTTGAGAAATAATACCATCCATGTGACCGAGAAATTACAAGATAACCAACACAGAC  
TGGACAAATGGTCTTTCAGAGACAGTTACACATCTGTGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTAUTGCCAGTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGAGGACCA  
GCTGTGTCTGGGGTCACTGACCAAAATGGCCACCAAGGGGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGCTGTGCTGTGCTTCCAGAGAGGCCGCTGTGTTCCCTGTG  
ACACCCCTGCCGTGGAGGGCGAGCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTGGACCGATGCCCTGTGCCAGTGGCTCCCTGCGCAGC  
CCCACAGCCACAGCCTGGTGTATGAGTGAAGGTTGAGGAGCTGAGGAGGAGGAGGAGGAGG  
GAGATCTGCTGCCAGAGAGGGTCCCCGATGAGTGAAGGTTGAGGAGCTGAGGAGGAGGAGG  
CCAGGGACTGGAGGACCTGGAGGGCCTGACTGAAGAGATGGCCTGGGGAGGCCGCTGCGCTG  
CCGCCGCTGCACTGCTGGGAGGGAGAGAATTTAGACTGGACCAGGCTGTGGTAGATGTGCAA  
TAGAAAATAGCTAATTATTTCCCCAGGTGTGCTTAGGGCTGGGCTGACCAGGCTTCTCCTA  
CATCTCTCCCAGTAAGTTCCCTCTGCTTGACAGCATGAGGTGTGCAATTGTTCACT  
CCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGCTGGGAGAGTCAGGCAGGGTAAACTGCA  
GGAGCAGTTGCCACCCCTGTCAGATTATTGGCTGCTTGCCTTACCAAGTGGCAGACAGCCG  
TTTGTCTACATGGCTTGTATAATTGTTGAGGGAGGAGATGGAAACAATGTTGAGTCTCCCTC  
TGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGTTGCAAACATCAACCTGGAAAAATG  
CAACAAATGAATTTCACGCACTTCTTCATGGCATAGGTAAGCTGTGCTTCAGCTGTTGC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTATTCACTCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATAATTCCCTCTCAGCACAGCCTGGG  
AGGGGGCATTGTTCTCTCGTCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCATCTGGTTGACTCTAAGCTCAGTGCCT  
CTCCACTACCCACACCAGCCTTGGGCCACAAAAGTGCCTCCAAAAGGAAGGGAGAATGGGAT  
TTTCCTGAGGCATGCACATCTGGAAATTAGGTCAAACATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGAGCCGTCTTAATGAAGACAATGAT  
ATTGACACTGTCCTTGGCAGTTGCAATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAAATTGTTAGGGCGAGGATTATAATGAAATTG  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACTGGAGAAAATCAAACCGAGCAGGG  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACACTCACGCCACTCCACAAATGAT  
TTTCAGGTGTATGGACTGTTGCCACCATGTATTCACTCCAGAGTCTTAAAGTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTCTTGTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAA  
ATCAAGCATAAAATCACTCAACTGCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAAAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVRREIHKITNNQTGQMFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRMCLTRDSECCGDQLCVWGHCT  
TKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRLLLITWELEPDG  
ALDRCPASCAGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAALLGSEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACGCGTGGCGGACCGTGGGGCTGTGAGAAAGGCCAATAAACATCATGCAACCCAC  
GGCCCACCTTGTGAACTCCTCGCCAGGGCTGATGTGCGTCTCCAGGGCTACTCATCCAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGTCTGGGCTCTCTGGACCCTT  
AACTGGGTACTGGCCCTGGCCAATGCGTCCTCGCTGGAGCCTTGCCTCCTACTGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTCCCCTTAATCTGCCTCATCCGCACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGGAGCCCTACCTGACCTTGCAAGATAGCCCAGGTACCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGCCCCTGCATCATGTGCTGTTT  
CAAGTGCCTGGTGTCTGGAAAAATTATCAAGTCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTCTCAGCCAAAATGCGTCATGCTACTCATGCGAAC  
ATTGTCAAGGTGGTCGTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGCTCTGCTTCTTCTCCGGTCGATCCGGGCTGGTAAAG  
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCTGGGGCCTAT  
GTCATGCCAGCGGCTCTCAGCTTCCGGATGTGTGGACACGCTCTCCTGCTTCC  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCTACTACATGTCAAAGAGCCTCTAA  
AGATTCTGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGG  
CCCTGATCCAGGACTGCACCCCACCCCAACGTCCAGGCATCCAACCTCACTTCGCTTACAGGT  
CTCCATTTGTGGTAAAAAAAGGTTTAGGCCAGGCGCCGTGGCTACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCCGGCGGATCACCTGAGTCAGGAGCTCGAGACCAGCCTGCCAACATGGTG  
AAACCTCCGTCTTATTAAAAACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCACTCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAACGCTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAAA  
AAGATTTATTAAAGATATTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKG LIQRSVFNLQIYGVGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLRNAYIMIAIYGKNFCVSAKNAFMILLMRN  
IVRVVVLDKVTDLLLFFGKLLVVGVGVLSSFFFSGRI PGLGKDFKSPHLYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNNGSLDRPYYMSKSLLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

## **FIGURE 11**

GCCCCGGCGCCGGCGCCGGCGCCCAGGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGGCGTCCTGCCTCTGCGCTCTGCCCCCTGCATCTGTGCAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTCCTCTTCCCTGGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTACAAGCTGCCCTGGGTGTGAGGAGGGGCC  
GGGATCCCCACCGCTGCAGGCCACATCGACTGTGGCTCCCTGCTGGCTACCGCGCTGTACCG  
CATGTGCTCGCCACGGCGGCCTCTTCTTACCCCTGCTCATGCTCGGTGAGCAGCA  
GCCGGGACCCCCGGGCTGCCATCCAGAATGGTTTGGTTCTTAAGTCTGATCCTGGTGGCCTC  
ACCGTGGGTGCCTTACATCCCTGACGGCTCCCTCACCAACATCTGGTCTACTTCGGCGTCGTGGG  
CTCCTTCCCTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTGCACACTCTGGAAACCAGCGGT  
GGCTGGGCAAGGCCGAGGAGTGCGATTCCCGCTGGTACGCAGGCCCTTCTTCACTCCTC  
TTCTACTTGCTGTCGATCGCGCCGTGGCGCTGATGTTCATGTAACACTGAGGCCAGCGGCTGCCA  
CGAGGGCAAGGTCTTCATCAGCCTAACCTCACCTCTGTGTCTGCGTGTCCATCGCTGCTGTCC  
CCAAGGTCCAGGACGCCAGCCCCAACCTGGGTCTGCTGCAGGCCCTCGGTACACCCATG  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCGAGCATTG  
TGGGCCCTCATCATCTCCCTCTGTGCACCCCTTCATCAGTCTGCGCTCTCAGACCAACCGGCAGGTG  
AACAGCCTGATGCAACGGAGGAGTGCACCTATGCTAGACGCCACACAGCAGCAGCAGCAG  
GGCAGCCTGTGAGGCCGGCCTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCC  
ACTTCTGCCCTGGTGTGGCTCACTGCACGTACATGATGACGCTACCAACTGGTACAAGCCGGTGAG  
ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGAGGGCTGCT  
CCTCTACCTGTGGACCCCTGGTAGCCCCACTCCTCTGCCAACCTGGTGCCTCTGGCTCGGTACAGCC  
CAGCCTGCCATCTGGTGCCTCTGCCAACCTGGTGCCTCTGGCTCGGTACAGCCACCTGCC  
CCCCACACCAATCAGGCCAGGCTGAGCCCCAACCCCTGCCAACCTGGCTCCAGGACCTGCC  
CTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGGCTGCCCTTCCTCCCTCCCTGGTGTGGCCATACAGCATCTGGATGAA  
AGGGCTCCCTGTCCCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACTCCCAC  
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGACCCCTGCC  
GACTTCGTGCCTTACTGAGTCTAAGACTTTCTAATAACAAAGCCAGTGCCTGTAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQVLVLLIDFAHAWNQRWLGKAE  
ECDSRAWYAGLFFFLLFYLLSIAAVALMFYYTEPSGCHEGKVFISLNLTFCVCVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCFLFISLRSSDHRQVNSLMQTECAPPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGTRKMISTWTAVWVKICASWAGLLLWTLVAPLLLNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## **FIGURE 13**

CGGGCCAGCCTGGGGCGGCCAGGAACCACCCGTTAAGGTGTCTCTCTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCATGCTCTGCAGAATATCCATTCCATCAACCCCACACAA  
CTCATGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTGTTGTCACCTTGACCTCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTCTGGCAGTTTCGATTTAAAGTGTAAACTTGCATATGCTGTCAG  
ACTGCGCCATTGGTGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTACTAGCAAAG  
TGATCCTTCGAAGCTTTCTCTCAAGGGGCTTTGGCATGTGCTGCCATCATTTCATTTCATC  
CTTGCCTGGATTGAGACGTGGTCCTGGATTCAAAGTGTACCTCAAGAACAGAGAAGAAAA  
CAGACTCCTGATAGTCAGGATGCTTCAGAGAGGGCAGCACTTACCTGGTGGCTTCTGATG  
GTCAGTTTATTCCCCCTCTGAATCCGAAGCAGGATCTGAAGAACGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTAGAACATGATCACTTTGTTAAATGTGAAAAACCCACAGAACAGTC  
ATCGAGGCAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAATGGTGAAGTC  
CACTGCTGGTTTATTGAACAGCTAAAGATTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTAGTGCCTGCCTGGCTGGTAAGGTAATGTCATGATTCACTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAACAGTCTGTGCTGTATTCTAAC  
AAAAGACTTAATATATTGAAGTAACACTTTTTAGTAAGCAAGAACCTTTTATTCAATTCAAC  
AGAATGGAATTTTTGTTCATGTCAGATTATTTGTTATTCTTTAACACTCTACATT  
TCCCTGTTTTAACATGCACATGTGCTTTGACAGTTAAAAAGTGTAAATAAAACTG  
ACATGTCAATGTGGCTAGTTTATTCTGTTGCATTATGTGTATGGCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAACATGTAAAATGTCACCAGACATTGTATTATT  
TTATCATGAAATCATGTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTGAAATGC  
ACAAAATGACTTAAACCATTCAATCATGTTCTTGCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWAIALT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCGACCCGCCAGGAAAGACTGAGG  
CCGC GG CCTGCCCGGGCTCCCTGCCGCCGCCCTCCCGACAGAAGATGTGCTCAG  
GGTCCCCTCTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGCCCTGGGTGCAAGGGCTGCCCAT  
CCGGCTGCCAGTGCAGCCACAGACAGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCCC  
CGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTGAGAACGGCATCACCATGCTGACGC  
AGGCAGCTTGCCTGGCTGCCGGCTGAGCTCCTGGACCTGTACAGAACCGAGATGCCAGCC  
TGCCCAGC GG GTCTTCCAGCACTGCCAACCTCAGAACCTGGACCTGACGCCAACAGGCTG  
CATGAATACCAATGAGACCTCCGTGGCTGCGGCCCTCGAGGCCCTACCTGGCAAGAA  
CCGCATCCGCCACATCCAGCTGGTGCCCTGACACGCTGACCGCCTCTGGAGCTCAAGCTGC  
AGGACAACGAGCTGCCGGACTGCCCTGGCTGCGCTGCCGCCCTGCTGCTGCTGGACCTCAGC  
CACAAACAGCCTCTGGCCCTGGAGCCCGCATCTGGACACTGCCAACGTGGAGGCCCTGCCGCT  
GGCTGGCTGGGGCTGCAAGCAGCTGGACGAGGGGCTCTCAGCCGCTTGCACACCTCCACGACC  
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTATCCGAGGCCCTCCGGGGCTGACG  
CGCCTGCCGCTGGCGGCAACACCCGATTGCCAGCTGCCGCCAGGCCCTGGCCGGCTGGC  
TGCCCTGCCAGGAGCTGGATGTGAGCAACCTAAGCCTGCCAGGCCCTGCCGCCCTCGGGCC  
TCTTCCCCCGCTGCCGCTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCCCTGAGC  
TGGTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGCCAGCCCTGAGGAGACGCCGTGCCA  
CTTCCCCCCAAGAACGCTGCCGGCTGCTCTGGAGCTTGACTACGCCACTTGGCTGCCAG  
CCACCACCACGCCACAGTGCCACCCACGAGGCCCTGGTGCAGGGAGCCACGCCCTTGCT  
TCTAGCTTGGCTCTACCTGGCTTAGCCCCACAGGCCGGCAACTGAGGCCAGGCCCTGCC  
CACTGCCCAACCGACTGTAGGCCCTGTCCTCCAGGCCAGACTGCCACCGTCCACTGCC  
ATGGGGCACATGCCACCTGGGACACGGACCCACTGGCTGCTTGCTGCCAGGCTTCAAG  
GCCCTGACTGTGAGAGCCAGATGGGCAGGGACACGCCAGGCCCTACACCGTACGCCAG  
GCCACCACGGTCCCTGACCCCTGGCATGCCGGTGAAGGCCACCTGCCGTGGCTGCC  
AGCGCTACCTCCAGGGAGCTCCGTGCAGCAGCTGCCCTCACCTATGCCAACCTATCG  
GGCCCTGATAAGCGCTGGTGAAGCTGCCACTGCTGCCCTGCCGTGAGTACACGGTCA  
GCTGCCGCCAACGCCACTTACTCCGTCTGTGTCATGCCCTTGGGCCGGGCGGGTGC  
GCGAGGAGGCCCTGGGGGAGGCCATACACCCCAAGCCGCTCCACTCCAACCACGCC  
CAGGCCGCCAGGCCACCTGCCGCTCCTATTGCCGCCCTGGCGCGGTGCTCTGCC  
GCTGCCGTGGTGGGGCAGCTACTGTGTCGGCGGGGCCATGGCAGCAGGCC  
ACAAAGGGCAGGTGGGGCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGT  
CCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGCTGAGTGTGAG  
ACTCATGGCTTCCCTGGACCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
GAGAGAGACAGGGCAGCTGGGGGGCTCAGCCAGTGAAGATGCCAGGCCCTCCTG  
ACACCACTGAAGTTCTCAGTCCCAACCTGGGGATGTGTCAGACAGGGCTGTG  
GGGCCCTGTTCCCTGGACCTGGCTCCTCATCTGTGAGATGCTGTGGCCAGCTG  
CTAACGTCCTCCAGAACCGAGTGCCTATGAGGACAGTGTGCCCTGCC  
CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCCATGCC  
TCCAGGGGCCACCTGGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGG  
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAACAAAAGAAACTGG  
TTTAGGAACATGTTTGTCTTTAAATATATATTTATAAGAGATC  
GGGAAGATGTTTCAAAACTCAGAGACAAGGACTTGGTTTGTAAG  
GGCTTTGTAAGAAAAAATAAAAGATGAAGTGTAAA

## **FIGURE 16**

MCSRVPLLLPLLLALGPGVQGCPSCQCSPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLKLQDNELRALPPLRPRLLLLDLHSNSLLALEPGILDGTANVE  
ALRLAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLPEDL  
AGLAALQELDVSNLSQLPGDLSGLFPRLLAARNPFCNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPKNAQRLLLEDYADFGCPATTTATVPTTRPVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPPQPDCCPSTCLNGGTCHLGTRHHACLCPEGFTGLYCESQMGOGTRPSPTP  
VTPRPPRSLTGLIEPVSPSTSRLVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASIAEY  
TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGEALPSGE  
CEVPLMGFPGPGLQSPHLAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,

594-600, 640-646

## **FIGURE 17**

GCAGCGCGAGGCGCGGTGGTGGCTGAGTCGTGGCAGAGCGAAGGCACAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGTGCGGTGCTGAGCTTGGCCTGGCGTCCTCGG  
ATGAAGAAGGCAGCAGGATGAATCCTAGATTCCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTTGATTCAAAGAAATCTGA  
ATTAGAACCTCTATTCAAGAACAGGAAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGAGTCCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTA  
CGGAAACCAGCTTGACGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGAGGGAAAGATGGCAGACTGTGGTGTG  
CTACAACTATGACTACAAAGCAGATGAAAAGTGGGGCTTTGTGAAACTGAAGAACAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGATGAAAATCCTTAATGAAAG  
CAATAAGAAAAGCCAAAAAAGAGAACATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATGCTCTTTATTGGTGTATTACTGCCACAGAATATCCAG  
GCAGCGAGAGAGATTTGAGAACGCTGACTGAGGAAGGCTCCCAAGGGACAGACTGCTCTGG  
CTTCTGTATGCCCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCTTGTATATTACAT  
TTGGAGCTTGGGGCAATCTAATAGCCCACATGGTTGGTAAGTAGACTTTAGTGGAGGCT  
AATAATATTAACATCAGAAGAATTGTGGTTATAGCGGCCACAACCTTTCAGCTTCATGATC  
CAGATTGCTTGTATTAAGACCAAATATTCAAGTGAACCTCCTCAAATTCTGTAAATGGATAT  
AACACATGGAATCTACATGAAATGAAAGTGGTGGAGTCCACAATTCTTAAATGATTAG  
TTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAAATGGCTCTTTAAATTCTGTAGTTG  
GAATTGTCAGAATCATTTCACATTAGATTATCATAATTAAAAATTCTTAGTTCA  
AAATTGTAAATGGTGGCTATAGAAAAACACATGAAATATTACAAATATTGCAACATGC  
CCTAAGAACATTGTTAAACATGGAGTTATTGTGCAGAATGACTCCAGAGAGCTACTTCTG  
TTTTTACTTTCATGATTGGCTGTCTCCATTATTCTGGTCAATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTCCATTGGTCAATTGCTACTTTCTTGCTAATTGG  
AAGATTAACTCATTAAATAAAATTATGCTAAAGATAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDESVKDHTTAGRVVAGQIFLDSEEESEL  
ESSIQEEDSLKSQEGERVTEDISFLESPNPNENKDYEPPKKVRKPALTAIEGTAHGEPCCHFPFLFLDK  
EYDECTSDGREDGRILWCATTYDYKADEKWGFCETEEEAKRRQMQEAEMMYQTGMKILNGSNKSQKR  
EAYRYLQKAASMNHHTKALERVSYALLFGDYLQPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGATTTAAGCCCATTCTGCAGTGGAAATTGATGAACATAGCAAGAGGACACCATTCTT  
GTATTATAACAAGAAAGGAGTGTAACCTATCACACACAGGGGGAAAAATGCTCTTGGGTGCTAGG  
CCTCCTAATCCTCTGGTTCTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCCAGAACTTTGAT  
AAAAAGGGATTCATGTAATCGCTGCCGTGACTGAATCAGGATCAACAGCTTAAAGGCAGA  
AACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAGAGGACTG  
CCCAGTGGTGAAGAACCAAGTGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTGGACTCATCAGTGTGACACTAAATATGCTCCTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGGAGGTGCCCTGCAATCGTGGAGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAAGGTTCAATGACAGCTTAAGACGGACATGAAAGCTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAAACTGGCAGATCCAGTAAAGGTAAATTGAAAAAAAC  
TCGCCATTGGGAGCAGCTGTCTCCAGACATCAAACAACATGGAGAACGTTACATTGAAAAA  
AGTCTAGACAAACTGAAAGGCAATAATCTATGTGAACATGGACCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAGTCTTCCCTAAGACTCATTATGCCCTGGAAAAGATGCCAAA  
TTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTGCAAGACTTTTATTGTTAAACAGAAA  
GCAGAGCTGGCTAACCCAGGCAGTGTGACTCAGCTAACCAATGTCCTCCAGGCTATGA  
AATTGGCCATTCAAGAACACATCTCCTTCAACCCATTCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTGTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGTATCCAGGGT  
CCCTGCTCAAGTTCTTGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCT  
GTATTTAGGCTTGGCTGCTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCTTCAAAATGA  
TCTTACCGTGGCCTGCCCATGCTTATGGCCCCAGCATTACAGTAACCTGTGAATGTTAAGT  
ATCATCTTATCTAAATATTAAAGATAAGTCAACCCAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGlisVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSLFPKTHYAAKGDAKIFWIPLSHMPAALQDFLLLQKAE LANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 21**

CTGAGGC GGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGTGCTCGCG  
CACTCGTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATAAATTGA  
CATTCAAGAAATATAATTCCATGCTATCAGTTTAGCTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTTCACAAAAACTTGCAAGGAGCATT  
TTCAAACCAAGACCTGTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTACTC  
ATCGACTGGAACATTCTTATATAAACCTCAAAAGACTTTACAGGGTACCTTAGTGGTT  
GCCAATCTGGCATGCTGAACAACGGGTATAAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTAGCCGAGCAGTACAAACACACAGCTCTAAATTGGAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCAAGAGGAATTAAAGAGTATATGCAAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAACAGATTAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA  
ACATTTCCTTGTCAAGCATTACGGACCTTTCCAAATTCTGAATTCTTCATTGATGTGTT  
ATGTCTTAAAAAATAGACATGTTCTAAAAGTAGCTGTAACATACACCACATCTGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAGCCTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAAGCATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTGGTGAATATTACGGTCTC  
CTACATTTGATCCTTAACCTTACAAGGAGATTTTTATTGGCTGATGGTAAAGCCAAAC  
ATTCTATTGTTTACTATGTTGAGCTACTTGCAGTAAGTCATTGTTTACTATGTCACC  
TGTTGCAGTAATACACAGATACTCTTAGTGCATTACTTCACAAAGTACTTTCAAACATCA  
GATGCTTTATTCCAAACCTTTTACCTTCACTAAGTGTGAGGGGAAGGCTACACAG  
ACACATCTTAAAGATACTGGAAAAGTGAGCAGCAGGACAGTGGCTCACACCTGTATCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGCAACGTATT  
GAGACCAGTCTATTAAAAAATGGAAAAGCAAGAATAGCCTTATTTCAAAATATGGAAA  
GAAATTATATGAAAATTATCTGAGTCATTAAATTCTCCTTAAGTGTGATACTTTTAAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVGWYKFRRHSDQIMTRERLLHKNLQEHSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFeedGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHSVSKSCNYNHLDVVDNLTL  
MVEHTDIPEASPASTPQIIKHKA  
LDLDDRWFQFKRSRLLDTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## **FIGURE 23**

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA  
GCAGCGCGCAGCGAACGCCGCCGCCACACCCCTCGCGTCCCGCGCGCCACCCCTCCCTCCCTCCCC  
GCGTCCCCGCCCTCGCCGCCAGTCAGCTTGCCGGTTGCTGCCCGCGAAACCCCGAGGTCAACCAGCCCGGCCCT  
GCTTCCCTGGGCCGCGGCCCTCACGCCCTCCTCTCCCGGCCGCGCTGGCACCGGGGACCGTTGCGCTGA  
CGCGAGGCCAGCTACTTTGCCCGCTCTCCGCCCTGCGCTTCCACCAACTCCAACCTCTTCTCCC  
TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGGCCGCTTCCCGTCCGGTCCAAA  
GGTGGGAACCGCTCCGCCCGCCCGACCATGGCACGGTCGGCTGCCGCTCTCGCACCCGGCAGTGC  
AGGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTGCTCGGAAGTGCAGCTTTACGTGCTCAAAGGCTC  
AACAGAACGATGCCCTCCACGAGATCAACGGTGTCAATTGAAAGATCTGCTCCCAGGGTCTACCTGCTGCT  
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTCAAAAGTGTGGTCAGCGAACAGTGAATCATTTG  
CAAGCTGTCTTGCTTCACTACAAGAGTTGATGAATTCTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTG  
AATGATATGTTGTGAAGACATATGGCCATTATACATGCAAATTCTGAGCTATTAAAGATCTTCGTAGAGTTG  
AAACGTTACTACGGGGAAATGTGAACACTGGAAGAAATGCTAAATGACTTCTGGCTGCCCTGGAGCGGATG  
TTCCGCCCTGGTAACCTCCAGTACCACTTACAGATGAGTATCTGGATGTGTGAGCAAGTATAACGGAGCAGCTGAAG  
CCCTTCGGAGATGTCCCTCGAAATTGAGGCTCAGGTTACTCGTGTGTTGTAGCAGCCGTACTTCGCTCAAGG  
TTAGCGGTTGCCGGAGATGTCTGAGCAAGGTCTCCGTGGTAAACCCCACGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCACTGCCGGGCTCGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGC  
TGTTTGGCCAACCAAGGGGATCTGATTTGAATGGAACATTCTAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCTTCACACATTGAATCGGTATGGATCCATCGATGTGAAGATTCTGATGCTATTATGAACATGCAGGAT  
AAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCAAGCCCCTCCAGCTGGACGAATTCTCGT  
TCCATCTGAAAGTCCCTCAGTGTCTCGTCAACCCAGGAACACAGCCAAACCACAGCAGCTGGCACT  
AGTTGGACCGACTGGTACTGATGTCAGGAGAACGAAACAGGCAAGAAATTCTGGCTCCCTCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTCAGGAAACGGCAATGAGGATGACTGTTGGATGGAAAGGCAAAGCAGGTAC  
CTGTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAAACCCAGAGGTCCAGGTTGACACCAGCAAACAGAC  
ATACTGATCTCGTCAAATCATGGCTTCTCGAGTGTGACCGAGCAAGATGAAGAATGCAATGCAATGGAACGACGTG  
GACTTCTTGATATCAGTGTGAAAGTAGTGGAGAAGGAAGTGGAGTGGCTGTGAGTATCAGCAGTGCCCTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCATGAGAAAGGCCAGCTGCTGGTGTCCCTGGGCA  
CAGGCCTACCTCCTACTGCTCTGCATCTGGTTATGAGAGAGGGAGATTAATTCTCAAACTCTGAG  
AAAAAGTGTCTACAAAAGTTAAAGGCACCGATTATCACTTTTACCATCTAGTGAACCTTGCTTTTTAAATGAA  
TGGACAAACATGTACAGTTTACTATGTGGCACTGGTTAAGAAGTGTGACTTGTGTTCTCATTGAGTTGG  
AGGAAAAGGGACTGTGATTGAGTTGGTCTGCCCTGGCAACCCAAACCATGTTAACAGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTGTGCTTGTGATTTCACCTCTATTATTTGTTGATGTTTTCTCATTGCTTGTGGTT  
TTTTTTCCAACGTGTGATCTGCCCTGGTCTTACAAGCAAACCAAGGGTCCCTTGGCACGTAACATGTACGTT  
TCTGAAATATTAAGTGTACAGAAGCAGGTTTATTTATGTTATCTTATTAAGAAAAAGCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKS KSCSEVRRLYVSKGF NKN DAPLHEINGDHLKICPOGST  
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMFVKTYGH  
LYMQNSELFKDLFVELKRYYVG NVNLEEMLNDFWARLLERMFR LVNSQYHFTDEYLECVSKYTE  
QLKPGFDVPRKLKLQVTRAFVAARTFAQGLAVAGDV VSKV SVNPTAQCTHALLKMIYCSHC RGL  
VTVKPCNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKV FQGC GPPKPLPAGRISRSI SEAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSLPSNV CNDERMAAGNGNE DCWNGKGK SRYLF A VTGNG LANQGN NPEV QV DTS  
KPDILILRQIMALRVMTSKMKNAYNGNDV DFFDISDESSGE GSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCAGCAGGGAACCTCCATTATATTCTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGCTCTAGCAGCCTGAATCCAGGGGTGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGCGCCAAGAATGTGAGTGCAAAGATTGGTTCTGAG  
AGCCCCGAGAAGAAAATTCTAGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACAAATGTCAGCTAAGAAGCTTGCTCTGCCTTGTAGGAGCTCTG  
AGCGCCCACTCTTCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAAGACACTC  
TTCTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAGCA  
TGTTTTCAAGATCATTGTTGTTGCTCTCTAGTGTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCTACCCAGGCTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCC  
AGCTAGTGTCAATTAAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTT  
AAATGTCAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISSLLLLPLMILMSMVSSSLNPGVARGHDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPDCDFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTCTGCTTCTTACCTGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCCGTGCAAAAGCTACTTCCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGAAGATGGAGAGCAAGAACGGGAGCTTCAGCCAG  
ATAAAGGGCTTACAGGAGCCTCCGGAAAGTGGCCCTACTGGAGCTGGCTGCCAACCGGAGC  
CAACTTCAGTTCTACCCACCAGGCTGCAGGGCACCTGCCTAGACCCAATCCCCACTTGAGA  
AGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGTGTGGCTCCATGGATGTGGTGGCTGCACACTGGTGCTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCTGCAGGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGCCTTCATGTGGCAGCAAGTTTC  
GAGCCCACCTGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGGATCTTGA  
GAACGCCAGTTCTCGAAATCAAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTCCAAGCTCCAAGGCACTCATTGCTCC  
TTCCCCAGCCTCAAATTAGAACAGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACCTA  
GCAGAAATGAGAGAACATTGATGTACCACTACTAGTCCCTCTCCCAACCTCTGCCAGGGC  
AATCTCTAACTCAATCCGCCTCGACAGTGA~~AAAAGCTCTACTTCTACGCTGACCCAGGGAGG~~  
AAACACTAGGACCCGTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCTC  
CCAATGTTGCCCTTCCCTCGTTCCATGGTAAAGCTCCTCTCGCTTCCCTGAGGCTACAC  
CCATGCGTCTCTAGGAACTGGTCACAAAGTCATGGTGCCTGCATCCCTGCCAACGCCCCCTGAC  
CCTCTCTCCCACTACCACCTTCCCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAATAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLTLPLHIMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRVRLPGGVLFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCAGAAAGTCTCTCTG  
CCACTGACGCCCCCATCAGGGATTGGGCCTCTTCCCCCTTCCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGTGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAACAGGGTAGTGGGTGGCTAGGGGGCTGCCCTATTAAA  
GTGGTTTTATGATTCTATACTAATTACAAAGATATTAAGGCCCTGTTCATTAAGAAATT  
GTTCCCTTCCCTGTGTTCAATGTTGAAAGATTGTTCTGTGTAATATGTCTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTC SQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 31**

GTTCGAATTCTTCAACTATACCCACAGTCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT  
CCTCCAAGCAAGTCATTCCCTATTTAACCGATGTGTCCCTAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAAATGTCGG  
GAAGAGATAACAATCCTGGCCTGTGTATCCTCGCATTAGCCTGTCTTGCCATGATGTTACC  
TTCAGATTCATCACCAACCCCTCTGGTTCACATTTCATGGTTATTTGGGATTGTTGTT  
TGTCTGCGGTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGTTGCTATCGTATCACAGGCATCACGGCAGTG  
CTGCTCGTCTGATTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTCCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTCTCTGGTCTCTGGTGGCTGTGCTGAGCCTGGAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGGAAATATAAGCCCCTTCGGGATTGGTACATGTGGTGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTGCGTGCCAGCAAATGACTATAGCTGGGCAG  
TGGTTACTTGTATTCAACAGAAGTAAAAATGATCCTCTGATCATCCCATCCTTCGTCTCTC  
TCCATTCTCTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCACTTAAATCTGTGGTGAG  
GATTCCGAGAATCATTGTCATGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTTGATGCTGACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTC  
AACCGAGATGCATATACTACAACGTCTATTAAATGGACAGATTCTGTACATCAGCAAAGATGC  
ATTCAAAATCTTGTCCAAGAACATCAAGTCACCTTACATCTATTAAACTGCTTGAGACTTCATAA  
TTTTCTAGGAAAGGTGTTAGTGGTGTGTTCACTGTTTGAGGACTCATGGCTTTAACTAC  
AATCGGGCATTCCAGGTGTGGCAGTCCTCTGTTATTGGTAGCTTTTGCTACTTAGTAC  
CCATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCTGTGTTTGCTGTTGATC  
TGGAAACAAATGATGGATCGTCAGAAAGCCCTACTTATGGATCAAGAACATTCTGAGTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA  
GGGAACAGAACCTCCAGGCCATTGTGAGAATGATACCCATTAGTACATGTACCTGGAAAACATT  
TCCTCTAAGAGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATT  
TTAAAGACCTAATAAACCTATTCTCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGILGLLFVCGLWWLYDYTNDSLIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPLLLQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA  
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMMQNALKQQHG  
ALSRYLFRCYCFCWCLDKYLLHLNQAYTTAINGTDFTSAKDAFKILSKNSHFTSINCQGD  
IIIFLGKVLVVCFVFGLMAFNYNRAFQWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNAQAQDKHSLRNEEGTELOQAIVR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

### **FIGURE 33**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTGGACCTCTCCCTGTTCTCCCTAGA  
ATAATTGTATGGGATTGTGATGCAGGAAGCCTAACGGAAAAAGAATATTCAATTCTGTGTGGT  
GAAAATTTTGAAAAAAATGCCCTCTCAAACAAGGGTGTCAATTCTGATATTATGAGGAC  
TGTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTCCTGTTTGCTGGTACTGGAGTAC  
ATTCAAACAAAGAACGGCAAAGAAGATTAAAGGCCAACGTTCACTGTGCCCTCAGATCAACTGC  
GATGTCAAAGCGGAAAGATCATCGATCCTGAGTTCAATTGAAATGTCAGCAGGATGCCAAGA  
CCCCAAATACCATGTTATGGCACTGACGTGATGCATCCTACTCCAGTGTGTGGCGTCCCG  
TACACAGTGGTGTGTTGATAATTCAACGGGAAATACTGTTGGAAGGTTGCTGGACAGTCT  
GGTTACAAAGGGAGTTATTCCAACGGTGTCAATTGTTATCCCTACACGATGGAGAGAAATCCTT  
TATCGTCTAGAAAGTAAACCAAAAGGGTGTAAACCTACCCATCAGCTTACATACTCATCAT  
CGAAAAGTCCAGCTGCCAACGAGGTGAGACCACAAAGCCTATCAGAGGCCACCTATTCCAGGG  
ACAAC TGCA CAGCGG TCA CTGATGCAGCTCTGGCTGTCACTGTAGCTGTGCCACCCCCAC  
CACCTTGCCAAGGCCATCCCCTCTGCTGCTTCTACCACCGATCCCCAGACCAACATCAGTGG  
GCCACAGGAGCCAGGAGATGGATCTGGTCCACTGCCACCTACACAAGCAGCCAAAAGGCC  
AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTCAGGAGCTGCCTCCAGAAACCTGTTGGAGC  
GGATGTCA CGCCTGGGACTTGTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCC  
TGGGAGATCCAAACTGCAAATGACTTGTGTTTAATTGATGGGAGCACCAGCATTGGCAAA  
CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTGCCAAGCTTGTGACATTGGCCCTGC  
CGGTCCACTGATGGGTGTTGTCAGTATGGAGACAACCTGCTACTCACTTAAACCTCAAGACAC  
ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTCTAAT  
GTAGGTCGGGCCATCCTTTGTGACCAAGAACTTCTTCCAAAGCAATGGAACAGAAGCGG  
GGCTCCAAATGTGGTGGTGTGGATGGCTGGCCACGGACAAAGTGGAGGGAGGCTTCAA  
GACTTGCAGAGAGTCAGGAATCACATTCTCATCACCATTGAAGGTGCTGTTGAAAATGAG  
AAGCAGTATGTGGTGGAGGCCAACTTGCACAAACAAGGCCGTGTCAGAACAAACGGCTTCACTC  
GCTCCACGTGCAGAGCTGGTTGGCCTCCACAAGACCCCTGCAGCCTCTGGTGAAGCGGGTCTGC  
ACACTGACCCGCTGCCCTGCAAGAACCTGCTTGAACCTGGCTGACATTGGCTCGTCATCGAC  
GGCTCCACCGTAGTGGGGACGGCAACTTCCGCACCGTCTCCAGTTGTGACCAACCTCACCAA  
AGAGTTGAGATTTCCGACACGGGACACGGCATCGGGGGCTGTGAGTACACCTACGAACAGCGG  
TGGAGTTGGGTTGCAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGG  
TACTGGAGTGGTGGCACAGCACGGGGCTGCCATCAACTTCCGCCCCTGGAGCAGCTTCAAGAA  
GTCCAAGCCCAACAAAGAGGAAGTTAATGATCCTCATCACCGAGGGAGGTCTACGACGACGTCC  
GGATCCCAGCCATGGCTGCCATCTGAAGGGAGTGTACACCTATGCGATAGGCCTGGCCTGGCT  
GCCCAAGAGGAGCTAGAAGTCAATTGCCACTACCCCGCAGAGACCACTCCTCTTGTGGACGA  
GTTTGACAAACCTCATCAGTATGTCCCCAGGATCATCCAGAACATTGATCAGAGTTCAACTCAC  
AGCCTCGGAACTGAATTCAAGAGCAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT  
GGACCAACCCACCGCTTAATGGGGACGCACGGTGCATCAAGTCTGGCAGGGCATGGAGAAC  
AAATGTCTTGTATTATTCTTGCATCATGCTTTTCAATTCCAAAATGGAGTTACAAGA  
TGATCACAAACGTATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTACAT  
TTTGACAATTGTTTCAAAATAATGTTGGAATACAGTGCAGCCCTACGACAGGCTTACGTAG  
AGCTTTGTGAGATTTAAGTGTATTCTGATTTGAACTCTGTAACCCCTCAGCAAGTTTCA  
TTTGTCATGACAATGTAGGAATTGCTGAATTAAATGTTAGAAGGATGAAAATAAAAAAAA  
AA  
AAG

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVTYDGYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGYSNGVQSLSLPRWR  
ESFIVLESKPCKGVTVPSALTYSSSKPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPPTLPRPSPSAASTTSIPRQPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQQRQDPSGAFAQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNCCCCMVWDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTQPLVKRVCCTDRCLACSKTCLNSADIGFVIDGSSSGTGNFRTVLQFVTN  
LTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAIAFAEQQL  
FKKSCKPNKRKLMILITDGRSYDDVRIPAMA AHLKGVITYAIGVAWAQEELEVIATHPARDHSFF  
VDEFNDLHQYVPRIQNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTGCCTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTTTCTGTTTCAGAGTAGTCACAACAGATCTGAGTGTTAATTAAAGCATGGAAT  
ACAGAAAACAACAAAAACTTAAGCTTAATTTCATCTGGAATTCCACAGTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTCCCGCTGGCTGCTATCACGTGGTGCCTCGACTACTCACCCGAGTGTA  
AAGAACCTCGGCTCGCGTCTGAGCTGCTGGATGGCCTCGGCTCTGGACTGCTCCCTGGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCGCTGCTGTCACCTCTGAGTTCTTGATGTGGTAC  
CTCAGCCTCCCCACTACAATGTGATAGAACCGTGAACGGATGACTCTATGAGTATGAGCCGATTAA  
CAGACAAGACTTCACACTCACACTCGAGAGCATTCAAACACTGCTCTCATCAAATCCATTCTGGTCATT  
TGGTGACCTCCCACCCCTCAGATGTGAAAGGCCAGGCCATTAGAGTTACTTGGGGTGAAGAAAAGCT  
TGGTGGGATATGAGGTCTTACATTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGC  
ATTGTCCTTAGAGGATGAAACACCTCTTTATGGCACATAATCCGACAAGATTTTAGACACATATAATA  
ACCTGACCTGAAAACCATTATGGCATTCAAGGTGGTAACGTGAGTTTGCCTAACGTAATG  
AAGACAGACACTGATGTTTCATCAAACTGGCAATTAGTGAAGTATCTTAAACCTAAACCAACTCAGA  
GAAGTTTCACAGGTTATCCTCTAATTGATAATTATTCCCTATAGAGGATTTACCAAAAACCCATATT  
CTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCATACTGCAGTGGGTGGTTATATAATGTCAGAGAT  
TTGGTGCCAAGGATCTATGAAATGATGGTCACGTAACCTCAAGTTGAAGATGTTATGTCGGAT  
CTGTTGAATTATTAAAAGTGAACATTCAATTCCAGAAGACACAAATCTTCTTCTATATAGAATCC  
ATTGGATGTCGTCAACTGAGACGTGATTGCAGGCCATGGCTTCTCCAAGGAGATCATCACTTT  
TGGCAGGTCATGCTAAGGAACACCATGCCATTTAACTCACATTCTACAAAAGCCTAGAGGACAG  
GATACCTGTGAAAGTGTAAATAAGTAGGACTGTGGAAAATTCACTGGGAGGTCACTGTGCTGGCT  
ACACTGAACCTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTAGTCAGG  
CCCTTCAAAGATGATATGTGGAGGAATTAAATAAGGAATTGGAGGTTTGCTAAAGAAATTAAATAGG  
ACCAAACAAATTGGACATGTCACTGTAGACTAGAATTCTTAAAGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGAAAAACAAACATGTAGAGTTATTGAAACAATGTAGTCACCTGAAGGTTTGCTGTA  
TATCTTATGTGGATTACCAATTAAAAATATGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATA  
CTGAACAAAATTTCACCTGTGTTGGTCATTATAAAAGTACTTCAGTCAAGATGTTGCAGTATTTCACAGTTATT  
ATTATTAAAATTACTTCACATTGTGTTAAATGTTGACGATTCAACAGATAAAAGGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACGTGATCAGTTATTATTGATAACATCACTCCA  
TTAATGTAAGTCATAGGTCAATTGCAATATCAGTAATCTTGGACTTGTAAATTTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNCNSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIHQDFLDTYNNLTAKTMAFRWVTEFCPNAKYVMKTDVDINTGNLVKYLL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIHIPEDTNLFPLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

## **FIGURE 37**

## **FIGURE 38**

MELGCWTQLGLTFLQLLISSLPREYTVINEACPGAEWNIMCRECCYEYDQIECVCPEGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRGDNDGQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQQNGEWSGKQPIKACREP KISDLVRRRVLPMQVSRETPLHOLYSAAFSKQKLQSAPTK  
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRTCLRTGKWSGRAPSCIPICGKIENTAP  
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTS FQESHITVAGWNVLADVRSPGFKN DTLRGVVSVVDSLLCEEQHEDHGIPVSVDNMFCA  
SWEPTAPS DICTAETGGIAAVSFPGRASPEPRWHLMGLVWSYDKTC SHRLSTAFTKVLPFKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

## **FIGURE 39**

GGTTCCATACCTCTCATCTGAGAACATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAAACGTGGCTTAATC  
TGAAGGTCTCACTCAAATTCTTGATCTACTGATTCTGGGGCATGGCAAGGTTGCTTAAGGAGCTTGGCTGG  
TTGGGCCCTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGAGAATGAAGGCGCTCTGTG  
TGGTCTGCGCTTGGCTCAGTCGTAACATGACAATGTGGCAACCTGCACCTCTGTATTCAAACACTGT  
AAGGTGCGTCCCACACGGCCTGACCAAAGAGATAGGAAGAGGCCTCACAAAGATGGCTGTCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCCCCCCAGAGGTTCTGCAGCTGCCACCATCTCTTAATGACAGACGAGCCTGGCTAGACA  
ACCTGCCTACGTGCTCGGCAGAGGACGGCAGGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAAGTA  
GGGCACGGCCCTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAAATTCAGAGCTTGGTGTCTCGAA  
GGACAAAGAGCGGGAGTGCAGTTGCAACCAGCCGACAGGGCAGGGAAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTCCAAGGTTGACACCTGATTCAGATGGTGAATTACAGCATCAAGATCAATCGAGTAGATCCAGTGA  
GCCTCTTATTAGGCTGGTGGAGGTAGCAGAACCCACTGGCCATATCATTATCAAACACATTATCGTGTGGG  
TGATGCCAGAGACGCCGGCTACTGCCAGGAGACATCATCTAAAGGTAACGGATGGACATCAGCAATGTCCCTC  
ACAACATACGCTGTGCGCTCTCGCCAGCCCTGCCAGGTGCTGCGCTGACTGTGATGCGTGAACAGAAGTCCGCA  
GCAGGAACAATGGACAGGCCCGGATGCCCTACAGACCCCGAGATGACAGCTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGACAGCTTGAATAAAACTGTCGGAGGTGGATGAGCTGGGTTTCATCTCAATGTGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GCCAGAAAGTGCAGCTCATCTGATTCAGGCCAGTGAAGACAGTGTTCACCTCGTGTGTCAGGTCGGCAGC  
GGAGCCCTGACATCTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCAGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCTACAATTACTGTCATGAGAACGGTGTAAATCTAAAAAGACCCCGTGAATCTCTG  
GCATGACCGTGCAGGGGAGCATCACATAGAGAACGGTGTGTTAGCCATCTATGTCATCAGTGTGAGCCGGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTGGTGAATGTGGATGGGTCGAACAGAGGTGACCC  
GGAGTGAGGCAGTGGATTATGAAAAGAACATCCTCGATAGTACTCAAGCTTGGAAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACACATGGCCCACCCAGTGAATGGTCCCCT  
GGGTCAATGTGGCTGGAAATTACACGGTGTGTATAACTGTAAGAGATTGTGTTACAGAAGAAACACAGTGGAAAGTC  
TGGGCTTCTGCAATTGAGGAGTTATGAGAACATCAATGGAAACAAACCTTTTCTCAAAATCATTGTGAAGGAA  
CACCAAGCATACAATGATGGAAGAATTAGATGTGGTGAATTCTCTGCTGTCATGGTAGAAGTACATCAGGAATGA  
TACATGCTGCTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAAACTATTGTTCTGGCTGGCACTT  
TTTTTAGAATCAATGATGGTCAAGAGGAAACAGAAAATCAAATAGGCTAAGAAGTGAACACTATATTAC  
TTGTCAGTTTATTTAAAGAAAGAACATGTAAAATGTCAAGGAAAGTATGATCATCTAAATGAAAGCCAGTT  
ACACCTCAGAAAATGATCCAAAAAAATAAAACACTAGTTTTCTGATGTGGAGGATTCTCATTAACACTAC  
AACATTGTTATTTTCTATTCAAAAGCCCTAAACAAACTAAAATGATTGATTTGATACCCACTGAATT  
CAAGCTGATTAAATTTAAATTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTAAATTACAGCT  
AAAATTTTAAATGCATTGCTGAGAACAGTGTGTTCATCAAACAAAGAATAATTTTCAAGAGTTAA

## **FIGURE 40**

MKALLLVLWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDCASLTATAPS  
PEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIQHRYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNNGQAPDAYPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVIFNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPEAAHLIQASERRVHLVVSRQRSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTITCHEVNNIQKDGPESLGMTVAGGASHREWDLPIYVISVEPGGVISRDRG  
IKTGDILLNVDGVELTEVSERSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
SDWSPSWVMWLELPRLYNCKDIVLRRNTAGSLGFCIVGGYEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLRLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## FIGURE 41

ACCAAGGCATTGTATCTTCAGTTGTCATCAAGTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACACGTAATAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGCGCTGACAGTGGTGGGGC  
CACCAAGCTAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTCC  
ATAAGACCCCTCATTTGGGAAAGGGAAAAACTCTGACTAATGAAGCATTCCACGAAGAAGGTAGAACTT  
GACAACGTCCCTCTGTGTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTCAAACCAGATCTCAC  
TTTGGAAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAG  
CTTTACAGAGGGTGCACCTCGTCCCCACCGGAACAGAGAGAAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCACTCCACCAGGCTGAAGG  
TAAAAAGTTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAACCCCTCAAGGAAGAAAATTGGG  
ACTGCTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGTACAGTTACAGTGGATATTGG  
GGGTGTACTGCCCTAACAGAGAGCAGTTTCAAGGTGAATGGATTCTCTAACAACTACTGGGAT  
GGGGAGGCGAAGACCGATGACCTCAGACTCAGGGTTGAGCTCCAAAAGAATGAAAATTCCCGGCCCTG  
CCTGAAGTGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTTACACCAACTGTCACGAGTCAGCTGGAGAACAGATGGTTGAGTAGTTGTTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTATATACACATCACAGTGGATTCTGGTTGGTGCATGACCC  
TGGATCTTTGGTGTGTTGGAAGAACTGATTCTTGTGCAATAATTGGCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCAATTGTTGAGCTGAATTTCCTTTGTATTTCT  
TAGCAGAGCTCTGGTGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTTTGAGGACTCTGGTGAAGGAGATTATTAAATTGAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTGCTCGCCAAGGTAGAA  
AGGTACGAAGATAACAATACTGTTATTCAATTCTGTACAATCATCTGTAAGTGGTGGTGTAGG  
GAGAAGCGTCCACAAAGAGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCCTCAGTGATGCCACCAGAGAAATACATTCTTATTAGT  
TTTAAAGAGTTTGAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACAT  
ATTAACATAATAATATGTCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGGRYRPQECKALQRVAILVPH  
RNREKHILMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFIHDV  
DLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGVTAALSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQSVRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCGCAGCCTGACCAGTGGCTCTGTTTCCCACAACAG  
ACGGGACAACCTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGGCCAGGGCCAGCTGGATGCCAT  
GTTCCAGAGGCAGAAGGAGGCAGACACCCACTTCCCCATCTGCATTTCGCTGCCGGCTGCTGTC  
ATCGATCAAAGTGTGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCGTCCCCTCCC  
TTCCCTTATTATTCCCTGCTGCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTGTT  
TCCAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCHRSKCGMCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTCCCCAACATGCCTCACCC  
TCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACGTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATAACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCCCATAATGGTCCATCCTCCCCATCTC  
CTGGAGATGGGAGAAAGTGTATGACCTTCATCTGCGTTGCCAGGAACCTGTCAAGCAGAACT  
TCTCAAGCCCCATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTCCCCCTCTGCTCAGTCTTTGACTGGGCTATTCTTG  
GTTTCTGAAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGTGGACATTGTCGGG  
AAACTCCTAACATATGCCCTGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGAAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGTATTCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFTTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKKNDSGIYYVGIYSSSLQQPSTQEVVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLFLVGLFLWFLKRERQEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCCTGCTGGTCTACTGCTGTTAGGAGTAGTTCATGCGATACCTCTAATGTCAGC  
TAGTTGAGGAAGACCAATTTCTCAAACCCCATCTTGCTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGCCATTCCAGCAACAAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACGAACTGGAATGTTCTTCATCATTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTTAAAGGTCCTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCATGTGAATTTCATGGAAAACATCAGTGACATTCATCCAGAATCTCAA  
CTTGCAGTGGTTTCAATGACTCTTGGCACCTCCACTGGTTCAAAACCCACCGTAACG  
ACACCATGGGGAGTGGCGGAGGACTCTAGTTCACTTCGATTTCGAAGAAAAACACATAGG  
CTTATCCACTTCTCAGTATTTTAGGCTATTGCTTGGAATTTGGAGGTCCTGTTTGGGCT  
CAGTCAGAGTAGTCATCGGTTCCTTGGGCTGTGTGGAGTCTAAGGCGAAAGTCAAATTG  
TGTAGTTATGGAAAAAATGTAAGTATCAGTAGTTGAAAAAAAAAAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLGVVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCGCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
**CATGGAGAGAGTGACCCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCCTGGAAGCCAATGACC**  
CATTTGCCAATAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGC GGAGGGCTCCTGGCATTGCTGGATCGCGGAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAACGAGCACAGTCCTGTACCTGAGAAGGCCATCCCACACTCATCACTCCAGGCTCTGCCA  
CTACTTGCT**GAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC**  
TCCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT  
TTCTGATCAGGAGGCTTCTTATGAATTAAACTCGCCCCACCCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALLEANDPFANKDDPFYYDWKNLQLSGLICGGLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGCACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAGATGAAGTTCCAG  
GGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGAGTGGGAGGCTGGCCCTGCAGAG  
CGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCTGGAGACGCCCTGA  
GCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCTGGCTCAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAAGCAGTGGCACTGGAGTCAGGCAGGTTCCAGGCTTGGCG  
AGCAGATGCTTGGCAACAGGGTCGGGAAGCAGCCATGCTCTGGAAACACTGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCGCCGGCTCTGGCAGGG  
GTGCCTGGCCACAGGGTGGCTGGAAACTCTGGAGGCCATGGCATCTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCAGGGCAATCCTGGAGGTCTGGGACTCCGTGGGTCCACGGATAACCCG  
GAAACTCAGCAGGCAGCTTGGATGAATCCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTGGGACCAACACTCAGGGAGCTGGCCAGCCTGGCTATGGTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGCAGCAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGGCTCACAGTCGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA  
CCTCCTGGGATCCAGCACGGCTCCTCCGGCAACCACGGTGGAGCGGGCGAGGAAATGGA  
CATAAACCCGGGTGTGAAAGCCAGGGATGAAGCCCGGGAGCAGGGAAATCTGGGATTCAAGGG  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTCTTG  
GAGGCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCATACTGTGAACTCTGAGACGTCCCTGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTTCATCAACTGGGATGCCATAAACAGGACCAGAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGGCCACACTCCCTCTAA  
AACACCAACCCCTCTCATCACTAAATCTCAGCCCTGCCCTGAAATAACCTTAGCTGCCCAACAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVP  
GHSGAWETSGGHGIFGSQGGLGGQQGQNPGGLGTPWVHGYPGNSAGSGMNPQGAPWGQGGNGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGSGSQGSSGSGSNGDNNNGSSSGS  
SSGSSSSGSSGGSSGGSSGNSGGSRGDGSESSWGSSSTGSSSGNHGSGGGNGHKGCEKPGNE  
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGGSGDNYRGQGSSWGGDAVGGVNTVNSETSPGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAGAGGTTGTGGGACAAGCTGCTCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCTGGCTACTCCCTGCTGCTGGTGTGGGCTCCTGGCT  
ACTCGCCCGCATCTGGCTTGACCTATGCCCTCTATAACAACGCGCCGGCTCCAGTGTTC  
CACAGCCCCAAAACGGAACCTGGTTGGGTACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGCCACCTATTCCCAGGGCTTACGGTATGGCTGGTCCC  
CATCCCCCTCATCGTTTATGCCACCCTGACACCATCCGGCTATCACCAATGCCCTCAGCTGCC  
TTGCACCCAAGGATAATCTCTCATCAGGTTCTGAAGCCCTGGCTGGAGAAAGGAACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCTTCCATTCAACATCC  
GAAGTCCTATATAACGATCTCAACAAGAGTCGAAACATCATGCTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGCTGGACATGTTGAGCACATGCCCTCATGACCTGGACAGTCTA  
CAGAAATGCATCTCAGCTTGACAGCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGGAGCTCAGTGCCCTGTAGAGAAAAGAGCCAGCATATCCTCCAGCACATGGACTTCTGT  
ATTACCTCTCCATGACGGCGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC  
GCTGTCATCCGGAGCGCGTGCACCCCTCCCCACTCAGGGTATTGATGATTTTCAAAGACAA  
AGCCAAGTCCAAGACTTGGATTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGAAAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGTCTGTACAAACCTTGCAGGCACCCAGAATACCAGGAGCGTGCC  
ACAGGAGGTGCAAGAGCTCTGAAGGACCGCGATCCTAAAGAGATGAAATGGGACGACCTGCC  
AGCTGCCCTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTCATC  
TCCCAGTGCACCCAGGACATTGTTCTCCAGATGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGTCCATCACAAACCAACTGTGTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGTTGACCCAGAGAACAGCAAGGGAGGTACCTCTGGCTTTATTCCCTTCTCCGCA  
GGGCCAGGAAC TGCA CGGGCAGGCGTCCGCATGGGGAGATGAAAGTGGCCTGGCGTTGAT  
GCTGCTGCACTCCGGTTCTGCCAGACCAACTGAGCCCCGCAGGAAGCTGAAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGGCCCTGAATGTAGGCTTGCAG**T**A**T**T**T**C**G**  
CCATCCACCTGTTTTGCAATTGTCATGAATAACGGTGCTGTCAAA

## **FIGURE 54**

MSLLSLPWLGRLPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRLQCFPQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGLLSGGDKWSRHRRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPEYIATILELSALVEKRSQHILQHMDFLYYLSDGRRFHAC  
RLVHDFTDAVIREERRTLPTQGIDDDFKDKAKSKTLDFIGVLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLRHPEYQERCRCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPVTWPDPVEVDPFRFPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGTGTGTTGCACTTACCCGTGTTCTGCCT  
TTGGTGGCATAACAAGGGACTTGCACTTATCTCTGCATTTGCAGTCTTGCATTGACGTGG  
TACAGCCTTCCTTCATACCAATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTCTGC  
ATAATTCATGGCCAGTTATGAAGCTTGGAAAGGCACTATGGACAGAACAGCTGGTGGACAGTTT  
GTAACATCTCGAAACCTCTGTCTTACAGACATGTGCCTTTATCTTGCAAGCAATGTGTTGCTT  
GTGATTGAAACATTGAGGGTTACTTTGGAAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGTTCTGTATCTTGAGTGGAAATCTTCCTCATGTACCTGTTCCCTC  
TCTGGATGTTGTCCCCACTGAATTCCCATGAATAACAAACCTATTCAACAGCAACAGCAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNKGALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

## **FIGURE 57**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCAACATGCTCTGTCTGCCCCGCTG  
TACGTGCCGTATCGGGAAAGCCCAGCCAGTTCACTTTCAGTCACTTTCAGTCAAGGGCTCCCTGCCAGCTGAAGTCC  
ATTTCAACTCATGTTCTCATCCCTCCAGGAATTCTCCACCTACCGCCAGTGGAAAGCAGAAAATTGACAACCT  
GGAGATAAGGACCTTGATGGCAGCTAGACTTGAAGAATTGTCATTATCTCAAAGATCATGAGAAGAAGACTGGAGG  
CTGGTTTAAGATTTGCAAAAGATAATGTCAGGCCATTGAGCCAGGAGATCATGCTCCTGCCGGACTG  
GGAGTCAGATACTGAAACAGCAGGAGAAAAATTCTCAAGAGCATGGATAAAACCGCAGCATGACCATTCGACTGG  
AACGAGTGGAGAGACTACCACCTCCTCACCCCGTGGAAAACATCCCGAGATCATCTACTGAAAGCATTCCACG  
ATCTTGATGTTGGGTGAGAACTAACGGTCCCGATGATTCAAGCTGGAGGAGGAGCAGACGGGATGTTGGAGA  
CACCTGGTGGCAGGGGGTGGGGCAGGGGGCTATCCAGAACCTCAGCAGGGGGCTTGACAGCTCAAGGTGCTCATG  
CAGGTCTCATGCCCGAACACATGGCATCTGGTGTGCTTCACTCAGATGATTGAGAAGGAGGGGCCAG  
TCACTCTGCCGGGCAATGGCATCAAGCTCTTAAATTGCCCCGATCATGAGCATTAACATTGCTGAGACAG  
ATCAAGCGCCTTGTGGTAGTGAACAGGAGACTCTGAGGATTCAAGAGAGGCTTGCGCAGGGTCTTGCAGGGCC  
ATCGCCCAAGAGCAGCATCTACCAATGGAGGTCTGAAGACCCGGATGGCCTGCCAGAACAGCCAGTACTCAGGA  
ATGCTGGAGATGCCAGGGAGGATCTGGCAGAGGAGGGGGTGGCCGCTTCAACAGGCTATGTCACCAACATGCTG  
GGCATCATCCCTATGCCCGCATGACCTTGAGCTCAAGAGACGCTCAAGAATGCCCTGGCTGCCAGACTATGCCAG  
AACAGCGGGGACCCGGCTTGTGCTCTGCCCTGGCCTGGCAGCATCTGGAGCTACCTGGCTGCCAGCTAC  
CCCCCTGGCCCTAGTCAGGACCCGGATGCCAGGCCAGGCTTCAATTGAGGGCGCTCCGGAGGTGACCATGAGCACCTC  
TTCAAACATATCTGCCGACCGAGGGGGCTTGGGCTGTACAGGGGCTGGCCCCAACATTCAAGGTCATCCCA  
GCTGTGAGCATCACCTGTCTAGAGAACCTGAGATCACCTGGGCTGCACTGCCGTGAGCTGGGGAGGGC  
CGGGCCAGGAGCTGGAGCTGCCATCTGGGCCCCAGCTGGGCTGCAAGGCCACTCTACCTTGTGAATGCCAACACT  
AAGCTGTCTCGAGCAAGCTGTGAAACCCCTAGCGCAGGCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
GTCCTGTCACCCAGCAGACCCCTCTGGTTGGCTTCAAGGAGACCCAGGCTTCACTTCTAGGGCTTCAAGGTGAGCAGG  
CTCAGGCTCACATGTGAAAGACAGGACATTTCAGCTGAGTGCCTGCCAATAGTGAGCTGGAGCTGGAGGCCGGCT  
TAGTTCTTCATTTCACCTTGCAGGAGCTGTGGCACGGCCCTGCCCCCTGCCCCCTGCTGCCGTGCACTCCCTGTG  
CTCTCTGCTGCCCTGCTGTAGGTAAGTGGAGGGGGCTACAGCCCACATCCCAACCCCTGCTCAATCCC  
ATAATCCATGATGAAAGGTGAGGTGAGCTACGGCTGGCCCTCCAGGCTGACTCTCCAAACCTACAGCATGAGGCCAACCTG  
TGTGAAGGAAAGAGGAAAGGAGCTGGCTTGTGCTACTGGCATCTGAGGCCCTGGCTGACTGAGCTGGGCTCTGGGCT  
CTTGGGAGTGCAGGGGGCTGGGCTGCCCTGGCTGCCAGAAGGCAAGTGTGGGCTCATGGCTCTGAGCT  
GCCCTGGACCTGTCAAGGATGGGCCAACCTCAGAACCAAACACTGTCCTTCACTGTGGCATGAGGGAGTGGAGCA  
CCATGTTGAGGGCGAAGGCCAGGGCTTGTGTTGAGGGGGAGGAAAGGCTGGAGGGCTTAATTATGG  
ACTGTTGGGAAAAGGGTTGTGCTCAGAGTGTGCTGAGCTGGCTGCCCTGGGCTCTGTCACCCAGAGGGGGGGGG  
GAGCAGGAGCTGGCTGACTGTCAGGTTGCTGAGCTGGCTGCCCTGGGCTCTGTCACCCAGAGGGGGGGGG  
GGGACCCAGCCCCACATTCACTTGTGCACTGCTGGAACCTATTATTTGATTATTTAACAGAGCTTATGCT  
AACTATTTTATAGATTGTTAATTATAGCTGTCAATTTCAGTTCAATTATTTATCATATTATGTTATGTT  
GATTGACCTTCCCAAGCCGGGCACTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGCGCTGAGTCACATCT  
GTCCAGAGAAAATTCTTGGGACTGGGAGGCAAAAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
GTGGGGAGGGCTTGGCCCGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
AACCTTGAGGTGAACTCAGTTATTCTGGCTGCCAGGGGTTCTTCTTCACTTCTGAGATGCAAGGCC  
TGAGGTGCCCTCACTGTGAAATTGTTGGTGGCGGGGGCTGGAGGAGGGTGGGGGCTGGCTCCGCTCCAGC  
CTTCTGCTGCCCTGCTAACATGCCGCAACTGGGACCTCACGGTTGCACCTCCATTCCACCAAGATGACCTGA  
TGAGGAAATTCTCAATAGGATGCAAGAGCATTAAGGAAATTGTTGATGCAACATATAACTGGAGTCGTC  
AAATTAAAGGAAATTGGACGTTAGAGTGTGCTATTAAAGCAGCCTCTAATAAGGAGGAGGAGGAGGAGGAG  
AAA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSYSTYRQWKQKIVQAGDKDLDG  
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK  
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMILDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## **FIGURE 59**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATA CGCTGGAACCTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACACTGTGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTGAACCTGACATCAAACTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTAGGCTTGGCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTCAGAGGCCGGACAGCAGTGTGCTGATCAAAGTGTAGTT  
GGCAATGCCCTTTGGCTGAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACCTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAAACTGGAGCCTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTCCCC  
CAGCCCACAGTGGCTGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC  
CAGCTTGAGCTGAACTCTGAGAAATGTGACCATGAAGGTTGTCTGTGCTCTACAATGTTACGA  
TCAACAAACACATACTCCTGTATGATTGAAAATGACATTGCCAAGCAACAGGGATATCAAAGTG  
ACAGAACGAGATCAAAGGGAGTCACCTACAGCTGCTAAACTCAAAGGCTCTGTGT  
CTCTTCTTCTTGCCATCAGCTGGCACTCTGCCCTCACCTGATGCTAAATTAAT  
GTGCCCTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAGATATGACCTAGTTTATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAGAAGCCAAGCAGAAGGCTCCAATATGAACAAGATAAT  
CTATCTCAAAGACATATTAGAAGTTGGAAAATAATTATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGGAGGACAGGGATAGTGCATGTTCTGTGCTGAAATTAGTTATATGTG  
TGTAATGTTGCTCTGAGGAAGCCCCTGAAAGTCTATCCAAACATATCCACATCTTATATTCCAC  
AAATTAAAGCTGTAGTATGTACCCCTAAAGACGCTGCTAATTGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACTTTATGATGCTTCAAAGGTGCCTGGCTTC  
TCTTCCAACTGACAAATGCCAAGTTGAGAAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTAAATAAAACTGAGCACCTTCTTTAAACAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVILGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFQOPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYLMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTAGAACATCACCATGGCCAGCTATCCTTACCGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAAGGAGCCCCCTCGGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCCCTGGTGGTTATGGGGTCTGCCCTGGAGGGCTTATGGACCACAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGATGTTCCCTCTGGAACCTCCAGGAGGACCATATG  
GCGGTGCAGCTCCGGGGCCCTATGGTCAGCCACCTCAAGTTCTACGGTGCCAGCAGCCT  
GGGCTTTATGGACAGGGTGGGCCCTCCAAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCACGGCTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
AAATGGGCTACAACCTGAGCCCCAGTTACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGCAACATCCGGCTCAGCTCGAGGACTTCGTCA  
CCATGACAGCTCTCGGATGCTTGACCCAAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTTCTTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGTGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATGCCACCA  
AAATAGTGAGGACCAGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCCAGGAGCAGGTCTGTAAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCGTATGCCAGTGGTGAATGTTCATCGGCCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAAGGCCATCTGTCAAACAGAGCCATTCTCCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAAGTGGCTGGATTCTGCCACACCCATAAAT  
CCTTGTGTGTTAACCTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTGGCCAGGCTCTGCCCTGCAGCTGGACCCCTCACTGCCTGCCATGCTCTGCTCGGCT  
TCAGTCCTCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTAATTGATTTTTTC  
ATTGGGCCAAAGTCCAGTGAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSTPGGGPYGGAAPGGPYGQPPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELQALVNCNWSSFNDETCLMMINMFDKTSGRIDVYGFSAWKFIQQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

### **FIGURE 63**

CAGGATGCAGGGCCCGTGGCAGGGAGCTGGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCCTTTGCCCGGAGCATCGGTGTTGGAGGAGAAAGTTCCAAAACCTCGGGACC  
AACTTGCCCTAGCTCGAACACCTCCACTGGCCCTCTAACACTGAACATCCGAGCCCCGC  
TCTGGACCCTAGGTCTAATGACTGGCAAGGGTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAAGGGTGCCTCCATCGTGGGGCTGCCTGCCATG  
GATTCCCTGGCCCCCTGAGGATCCTGGCAGATGATGGCTGCTGCCGTGAGGACGCCCTGGGGGA  
AGCGCTGCCCTGAAGAACTCTTACCTCTCCAGTGCTGCCGTCCGGCAGTGGCCCTT  
TGCCTGGGAGTCTCTCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCGTCTAATTCACTGGAGCCGGGGAAAAATCCTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTCTGCCTGATCACCCCTGGGTACCTGAATCCCAAGT  
TGTCCCTGGGAGGTGGAGGCCCTGGACTGGTGGGAACGAGGCCATGCCACACCTGAGGG  
ATCTGGGGTATCAATAATCAACCCCCAGGTACAGCTGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGAGCTGGGAAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGAAATATTCTATACCCAGGTATCAATAACCCATTCCCTGGAGTTCTCCGC  
CCTCCTGGCTTCTGGAACATCCCAGTGGCTCCCTAATCTCCAAGCCCTAGGTGCACTG  
GGGCTAGAGCACGATAGAGGGAAACCCAACATTGGAGTTAGAGTCTGCTCCGCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTCCAGCACTATCCCCACTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPAGGSQRWPPSWGLPAMDSWPEDPWQMMAAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTWGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCTTGCTCCTCTTGACCCCTCTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGCTTTCTGACAAATTCCCTCATGAGTCCAGCTTCCGGAA  
TTGCTTGAAAAGCTCTGCCTCCCTCCATCTCCCTCAGGGACCAGCGTCACCCCTCACCATGC  
AAGATCTAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTGGCCC  
GGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAATAAATTCTGGTATGCTG

## **FIGURE 66**

MGSGLPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGC  
CAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGTAGGGAGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCGCCACCCAGCCCATGGCGAACCCGGGCTGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCGCTGGGCGAGGCTGGGGCAAAATACAGACCACCTCTGC  
AAATGAGAATAGCACTGTTGCCCTCATCCACCAGCTCCAGCTCCGATGGCACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTGGCTGCCTGCTCCTGGCTGTGGGCTG  
GCACTGTTGGTGCAGGCTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCCTCTGCATCTGTCTCCCTCATTGCTGTGACCTTGGGAAA  
GGCAGTGCCCTCTGGGAGTCAGATCCACCCAGTGCTTAATAGCAGGGAGAAGGTACTTCAA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGTLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQF~~SHAAE~~ARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

## **FIGURE 69**

GCCAGGAATAACTAGAGAGGAACAATGGGTTATTCAAGAGGTTTGTCTCTAGTTCTGCTGCTGACCAG  
TCAAATACCTCCTCATTAAGCTGAATAATAATGCCCTGAAGATATTGTATTGTTAGATCTAGTGTGCCAGAA  
GATGAAAAAATAATTGAACAAATAGAGGATATGGTACTACAGCTCTACGTACCTGTTGAAGCCACAGAAAAAAGA  
TTTTTTTCAAAAATCTATCTATTAAATTCTGAAGATTGAGAAATCCTCAGTACAAAAGGCCAAAACATGAA  
AACCATAAACATGCTGATGTTATAGTTGCACCCACACTCCAGGTAGAGATGAACCATACCCAAGCAGTTACA  
GAATGAGAGAGAAAGGGAAATACATTCACTCACCCTGACCTCTACTTGGAAGAAAACAAAATGAATATGGACCA  
CCAGGCAACTGTTGTCATGAGTGGGCTCACCTCGGTGGGAGTGTGATGAGTACAATGAAGATCAGCTTC  
TACCGTCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGAGGTATCTGGTAGAAATAGAGTTATAAGTGT  
CAAGGAGGCAGCTGTCTTAGAGCATGCAGAATTGATTCTACAACAAAATCTGTTAAAGGATTTGTCATTCTTT  
CCTGATAAAGTACAAACAGAAAGGATCCATAATGTTTATGCAAAAGTATTGTTCTGTTGAATTGTAACGAA  
AAAACCCATAATCAAGAAGCTCAAGGCTACAAAACATAAAAGTCAATTTAGAAGTACATGGGAGGTGATTGCAAT  
TCTGAGGATTAAACACATACCCATGTCACCCACTCTCCACCTGTCATTCTCATTGCTAAGATCAGTCAA  
AGAATTGTTGCTTAGTCTGATAAGTCTGGAAGCATGGGGGTAAGGACGCCAAATCGAATGAATCAAGCAGCA  
AAACATTCTGCTGCAGACTGTTGAAATGGATCTGGGTGGGATGTTCACTTGTAGTACTGCCACTATGTA  
AATAAGCTAATCCAAATAAAAGCAGTATGAAAGAACACACTCATGCCAGGATACCCACATATCTCTGGGAGGA  
ACTTCCATCTGCTGGAATTAAATATGCAATTCTCAGGTGATTGGAGAGCTACCTTCAACTCGATGGATCCGAAGTA  
CTGCTGCTGACTGATGGGAGGATPAACACTGCAAGTTCTGATTGATGAAGTGAACAAAGTGGGCATTGTCAT  
TTTATTGCTTGGGAAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTGTTGTT  
TCAGATGAAGCTCAGAACAAATGGCCTCATGATGCTTGGGCTTACATCAGGAATACTGATCTCTCCAGAAG  
TCCCTCAGCTGCAAAGTAAAGGATTAACACTGAATGTAATGCCCTGATGAACGACACTGTCATAATTGATAGTACA  
GTGGGAAAGGACACGTTCTTCATCATGGAAACAGTCTGCCCTCCAGTATTCTCTGGGATCCCAGTGGAAACA  
ATAATGAAATTTCACAGTGGATGCAACTTCCAAAATGGCTATCTCAGTATTCCAGGAACGCAAGGTGGCACT  
TGGGCATACAATCTCAAGCCAAGCGAACCCAGAACATTAACTATTACAGTAACCTCTGAGCAGCAAATTCTCT  
GTGCCCTCAATCACAGTGAATGCTAAATGAATAAGGACGTAACAGTCTCCCGAGCCAATGATTGTTACGAGAA  
ATTCTACAAAGGATATGACCTGTTCTGGAGCCAATGACTGCTTCTATTGATACAGAACATGGACATACAGAAGTT  
TTGGAACCTTGGATAATGGTGCAGGGCTGATTCTCAGGAATGATGGAGTCTACTCCAGGTATTACAGCATAT  
ACAGAAAATGGCAGATATGCTTAAAGTCTGGGCTCATGGAGGAGCTCAGGCCAACAGCATCCGGAGGTGCAATTGAT  
GAGGATACTCAGACCACCTGGAGGATTCTGCCGAACAGCATCCGGAGGTGCAATTGTTACAGTCCAAGC  
CTTCCCTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACACTTCAGGATAAGTATTCTT  
ACATGGACAGCACCAGAGATAATTGATGTTGAAAAGTCAACGTTATATCATAGAATAAGTCAAGTCCAAGTATTCTT  
GATCTAAGAGACAGTTGATGCTCTCAAGTAATACTGATCTGTCACCAAGGAGGCCAACTCCAAGGAA  
AGCTTGCATTAAACAGAAAATATCTCAGAAGAAATGCAACCCACATATTATTGCTTAAAGTATGATAAA  
AGCAATTGACATCAAAGTATCCAACATTGCAACAGTAACCTTGTATTCCCTCAAGCAAATCTGATGACATTGAT  
CCTCACACTCTACTCCACTCTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGGTATTG  
TCTGTGATTGGGCTGTTGAACTTGTGATTGATGCAACAGTTCTGAATTGACGAAACGTTGAACTTAAAGGAGGAA  
AAGTAGACCTAGAGAGACTTTAAAACAAAATCAATGTAAGTAAGGATACTTGTGATTAAATAAAACACTCATGGATA  
GTGAAAAACTGTCAAGATTAAATTAAGATGTCGGAAAAGGATACTTGTGATTAAATAAAACACTCATGGATA  
ATCCTTTTCAACTGATACCTGGTTGATATTGATGCAACAGTTCTGAATGATATTCAAAATTGCACTCAA  
GAAATTAAAATCATCTGAGTAGTCAAAATACAAGTAAAGGAGGAGCAATAACAAACATTTGGAAAAAAA  
AAA

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTFIKLNNGFEDIVIDPSVPEDEKIIEQIEDMVTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKEY  
IHFTPDLGGKKQNEYGPPGKLFWHEWAHLRGVFDEYNEDQPFYRAKS KIEATRC SAGISGRN  
RVYKCQGGSCLS RACRIDSTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVSLLKISQRIVCLVLDKSGSMGGKDRLNR  
MNQAAKHFLLOQTENG SWGMVHF DSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDGSEVLLTDGEDNTASSCIDEVKQSGAIVH FIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDA FGALTSGNTDLSQKSLQLESKGTLNSNAWMNDVIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAKM NDKVNSFPSPMIVYAEILQGYVVLGANVTAFIESQNGHTEVLELLDNA  
GADSFKNDGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRRPLNRAAYIPGWVVNGEIEANPP  
RPEIDEDTQTTLED FSRTASGGAFVVSQVPSLPLDQYPPSQTDL DATVHEDKIILTWTAPGDN  
FDVGKVQRYIIRISASILDLRDSFDDALQVN TDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPDKSHNSGVNISTLVLSVIGSVVI  
VN FILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## **FIGURE 71**

CTCCTTAGGTGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACTGCCCGGGCAGGGGTGA  
CAACAGGTGTCATCTTTGATCTCGTGTGGCTGCCCTCTATTCAAGGAAGACGCCAAGGTAATTGACCCA  
GAGGAGCAATGATGTAGCCACCTCTAACCTCCCTCTTGAAACCCCCAGTTAGGCCAGGATTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGCTCCCTCGCTTAACCTGTGGTTGGAGGAGAACCTTGTGGGCTGCCCTCTTAGCA  
GTGCTCAGAACTGACTTGCCTGAGGGTGGAGCAGAAAGAAAAGGTCCCTCTTGCTGTGGCTGCACATCAGGAA  
GGCTGTGATGGGATGAAGGTGAAACATGGGAGATTCACTTCAGTCATTGCTCTGCCCTGCAAGGATCATCCTTAA  
AGTAGAGAAGCTGCTCTGTGTGGCTTAACCTCAAGGGCAGAACCTCTAGAAGGAATGGATGCAAGCAGCTC  
CGGGGCCCAAACGCATGCTCTGTGGCTAGGCCAGGGAAAGCCCTCCGTGGGGCCCGGTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCTGAAATGATGATGGTTGCCGGGCTGCTGCGTGGATTTCCGGGTGGT  
GTTTGCTGGTCTCTCTGCTGTGCTATCTGCTGTGATCATGTTGGCTGCCACCCAAAAGGTGACGGAGGCAG  
CTGGCAGTCCCAGGGCACAGGCCAACGGGAAGGGGATCAGGGCTCCTCAGGAGTGGAGGAGCAGCAC  
CGCAACTACGTAGCAGCCTGAAGGGCAGATCGCAGACTCAAGGAGGAGCTGAGGAGAGGAGTGAGCAGCTAGG  
AATGGCAGTACCAAGGCAGCGATGCTGCTGGCTGGCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCACCTC  
CTGGCCTCCCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCTCAAGTGGCCACAGAGTATGCAGCAGTG  
CCCTTGATAGCTTACTACAGAGGTGACCTGGAGACTGGCTTACCCCGACGGGAGAGCTGTG  
AGGAAGGACAAGGGATGAGTTGGAGACCTGAATCAGCCTTGGAGACCTGAAACATCTGCAGGAGAACAGC  
CCCAATCACCCTCTAACGGCTCTGATTCTAGAAGGGATCTACCGAACAGAAAGGGACAAGGACATTGTAT  
GAGCTCACCTCAAAGGGACCAAAACAGAATTCAAACGGCTCATTTGACCATTCAGCCCCATCATGAAA  
GTGAAAAATGAAAGCTAACATGGCAACACGTTATCAATGTTATGTCCTAGCAAAAGGGTGGACAAGTTC  
CGGCACTCATGAGAAATTCAAGGGAGATGTCAGTGGAGACTGGCTGACGAGTGGAGACTGGCT  
AAAGAAGAAATAATGAAGTCAAAGGAATACTTGAACACTTCCAAGTGCACACTCAGGAACCTTACCTC  
CAGCTGAATGGAAATTCTCGGGAAAGGACTGATGTTGGAGCCCTCTCGAAGGGAGCAACGTCTTCTC  
TTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCTCAATACGTGAGGCTGAATACACAGCAGGGAGAAG  
GTATTTATCCAGTTCTTCAGTCAGTACAATCTGGCATATAACGGCCACCATGATGCACTCCCTCCCTGGAA  
CAGCACTGGTATTAAGAGGAACTGGATTGGAGAGACTTGGGATGACGAGTGTCACTGGTCAAGAC  
TTCATCAATATAGGTGGTTGATCTGGACATCAAAGGCTGGGGAGAGATGTCACCTTATGCAAGTATCTC  
CACAGCAACCTCATGTCAGGACGGCTGCGAGGACTCTCACCTCTGGCATGAGAACGGCTGCATGGAGG  
CTGACCCCGACAGTACAAGATGTCAGTCAGGCTGAACAGGAGCATCCACGCCAGCTGGCATGCTG  
GTGTTCAAGGACAGATAGGGCTCACCTCGCAAACAGAAACAGAACAGAACAGTAGCAAAACATGACTCCCA  
GAAGGATGTGGAGACACTTTCTCTCTGGCAATTACTGAAAGTGGCTGACACAGAGAAAAGACTTCAATAA  
GGACGACAAAAGAATTGGACTGATGGGTCAAGAGATGAGAAAGCTCCGATTCTCTGTTGGGTTTACAACAGA  
AATCAAAATCTCGCTTCTGCAAAGTAACCGATGTCACCTCTGAAGTGTGACAAAGGAGAATGCTGTG  
AGATTATAAGCTTAATGGTGTGGAGTTGATGGTTTACAATACACTGAGACCTGTTGTTGTCATTG  
AATATTGATTAAGAGCAGTTTGTAAAAATTCAATTAGCATGAAAGGCAAGCATATTCTCTCATATGAATGA  
GCCATCAGCAGGGCTAGTTCTAGGAATGCTAAATATCAAGAAGCAGGAGGAGATGAGCTTATTGACT  
AGTGAGTACATTAAGTAAATAAAATGGACAGAAAAGAACATTAATGTCATATTCTCCAAAG  
TAACCAAAAATCTGTTATCTTGGTCTCTTTAACTGTCCTTTTCTCTTATTAAAATGCACT  
TTTTCTCCCTGTGAGTTAGTCCTTAAATTACCACTTGCACGCCCTAACAGAGACACAATTGGCTAC  
ATTTTATATTAAAGAAGATACTTGAGATGCAATTGAGACCTTCAGTCACAGCATCAAATTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGCAAGCAGTAAATGCAAGGCTGAGACATAGGGAGGAATGTTTGTACT  
AATACAGACGTACAGACTTCTGTAAGAGTATTTCGAAGAGTATTGCAAGAGGAGAACACTGGAGGAAAAGAAATGAC  
ACTTTCTGCTTACAGAAAAGGAACTCATTCAAGACTGGTGAATCTGTCAGTACCTAAAGTCAGAACACATTT  
CTCCTCAGAAGTAGGGACGGCTTCTACCTGTTAAATAACCAAGTATACCGTGTGAACCAAACATCTTT  
AAAACAGGGTGTCTCTGGCTTCTGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATTGT  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGCTACATGTTATCCACCCAGGCCAGGGAG  
TAACTGAAATTTTAAATAACAGTTAACATAGGTTCTTCACTCATGAAATTTGCACTTATTACCATTT  
CAAACATTTTAAATAACAGTTAACATAGGTTCTTCACTCATGAAATTTGCACTTATTACCATTT  
ATTCAAGCTGTTGGTGTGTTAAAATGCAATTGATTGATTGACTGGTAGTTATGAAATTAAACACAGG  
CCATGAATGGAAGGTGGATTGCAAGCTAATAAAATGATTGATGGATATGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVVLLVLLCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIESALETLNNA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKEFKRLILFRPFSPIMKVKNEKLNM  
TLININVPLAKRVDKFQFMQNPREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLF  
NPGIIYGHDAVPPLEQQLVVIKKETGFWRDFGFGMTQYRSDFINIGGFDLIDKGWGGEDVHLYR  
KYLHSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAH  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

## **FIGURE 73**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTGGGATCCA  
GAAACCCATGATAACCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGACAGCAAGA  
GAAGCAGAGATAAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCACTCCTC  
CCTCCCTCTCTCTGCCCTGTCCTAGTCCTAGTCCTAAATTCCAGTCCCTGCACCCCTC  
CTGGGACACTATTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCTGGCTGCAGATGGG  
GTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGCCAGCCTTACCTGAGTGT  
GGAAACAATGCCAGTCGCCATCGATATTCAAGACAGACAGTGTGACATTGACCCCTGATTGCC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTGCAACTCTCTGCCCTCACCCCTGTATCTGGGTGGACTTCCCGAAAAATATGTAGCT  
GCCAGCTCCACCTGCACTGGGTCAAGAAAGGATCCCCAGGGGGTCAGAACACCAAGATCAACAG  
TGAAGCCACATTGAGAGCTCCACATTGTACATTGTACTCTGATTCTATGACAGCTTGAGTGT  
AGGCTGCTGAGAGGCCCTAGGGCTGGCTGCCTGGCATCCTAATTGAGGTGGTGAGACTAAG  
AATATAGCTTATGAACACATTCTGAGTCAC TGATGAAGTCAGGCATAAAGATCAGAACACCTC  
AGTGCCTCCCTCAACCTAACAGAGAGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTTGCTACCAGAGTGTGCTGGACAGTTTTATAGAAGGTCCAG  
ATTCAATGGAACAGCTGGAAAAGCTTCAGGGACATTGTCACAGAGGATCTGGCTTCTAA  
GCTTCTGGTACAGAACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCA  
TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTTAGGAATCTGGTTGGC  
TGTCTGCTCTGGCTTCTGGCTGTTATTCAATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAA  
CCGAAAGAGTGTGGCTTCACCTCAGCACAGCCACGACTGAGGCATAAATTCTTCTCAGATA  
CATGGATGTGGATGACTCCCTCATGCCATCAGGAAGCCTCTAAATGGGTGTTAGGATCTGG  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTCTTAGAGAGGAAT  
GGACCCAGGCTGTCAATTCCAGGAAGAACTGCAGAGCCTCAGCCTCTCAAACATGTAGGAGGAA  
ATGAGGAAATCGCTGTGTTATGCAGAGANAAACTCTGTTAGTTGCAGGGGAAGTTGG  
ATATAACCCAAAGTCTCTACCCCCCTCACTTTATGGCCCTTCCCTAGATATACTGCGGGATCT  
CTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTGATCAATATAATTGGAAATTAAAG  
TTTCTGACTTT

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGACGGGCAGTCCCTGTGTC  
TCTGGGGTTGCCCTAAACCTGCAAACATCACCTTATCCATCAACATGAAGAATGCCTACA  
ATGGACTCCACCAGAGGGCTTCAAGGAGTTAAAGTTACTACACTGTGAGTATTCCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAACGTCATTCTGTGCTGACAGCTCC  
AGAGAAAGTGGAAAGAAAATCCAGAAGACCTCCTGTTCCATGCAACAAATAACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCAGTGTGACCAACCAC  
ACGCTGGTGTGTCACCTGGCTGGAGGCCAACACTCTTACTGCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTGCCGTGCTCAGCCTCTGAGAACAGCAGTGTGCCAGGACTTGAAAGATCAATCAT  
CAGAGTCAAGGCTAAATCATCTTGTGGTATGTTGCCATATCTATTACCGTGTGTTCTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTGGAAAGAGAAACACCCAGCAAATT  
GATTTGATTTATGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGAAAAAAATCGTGATTA  
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAATTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCCAGGGAACCTGAGGCCCTCAGGAA  
GGAAGAGGAGGTGAAACATTAGGGTATGCTTCGCAATTGATGGAAATTGGTGA  
AAAACACGGAAGGTACTTCTCACCCAGCAAGAGTCCTCAGCAGAACAAACCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACACTGACATTGTGCGGGGCCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTGGCAG  
TCTTGGGCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGC  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATGACGACCCGGTGCAGGG  
TCCCCAAACTGGCAGGCTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTAGGAGGGCTGCG  
AGCCTTCTGAGGGGATGGGCTCGAGAGGAGGGCTTCTATCTAGACTCTAGGAGGCCG  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGTTATA  
TGTGCAGATGGAAAACTGATGCCAACACTTCTTTGCCCTTGTGCTGAAACAAGTGAG  
TCACCCCTTGATCCCAGCATAAAAGTACCTGGGATGAAAGAAGTTTCCAGTTGTCA  
CTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTGGTCATGCATGTA  
GGTCTCTAACATGATGGTGGGCCTCTGGAGTCCAGGGCTGGCCGGTGTCTATGCAGAGAA  
AGCAGTCATAAATGTTGCCAGACTGGGTGCAGAATTATTAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILLYGNEFDKRFFVPAEK  
IVINFITLNISDDSKISHQDMSSLGKSSDVSSLNDPQPSGNLRPPQEEEVKHTMLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQLSLQEEVSTQGTLLESQA  
ALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSFDQDS  
EGCEPSEGDLGEEGLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQmen

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## **FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCAC TTGCTGCCCTTGACAC  
CTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTCTGTGGTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTCACTACAGCTAACATCCTCCAGCTGCAGGTGAAGGCCCTGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCACCCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACTGCTGTA  
TAAGCTCTCCTTCCTGGTGAACGCCCTAGCTAAGCAGGTCACTGAACCTCTAGTGCCTACCCCTGC  
CCAATCTAGTGAAAAACCAGCTGTGTCCTGATCGAGGCTCTCAATGGCATGTATGCAAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTCCCTCAGCATTGACCGTCTGGAGTTGACCTTCTGTA  
TCCTGCCATCAAGGGTGAACCCATTCAAGCTCACCTGGGGCCAAGTGTGACTCACAGGGAA  
AGGTGACCAAGTGGTCAATAACTCTGCAGCTCCCTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTAGTCAGGACGTGGTGAAGAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGA  
ATTCACTGGCCTGTGGACTCTGTGCTTCTGAGAGTGCCCCTGCGCTGAAGTCAGCATCGG  
TGATCAATGAAAAGGCTGCAGATAAGCTGGATCTACCCAGATCGTAAGATCTTAACCTCAGGAC  
ACTCCCCAGTTTTATAGACCAAGGCCATGCAAGGTGGCCAAGTGTGCTGGAGCT  
TCCCTCCAGTGAAGGCCCTCCGCCCTTGTTCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTGCTTGTGAAGG  
CCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAAGGCTGG  
GTCCCAGCTGGAGTATGGGTGTGAGCTCTAGACCATCCCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK  
PAGGIPVLGSLVNTVLKHIWLKVITANILOLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLDSQGKVT  
KWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTKDALVLTPASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCA~~ACT~~TGTGGGCTACATCCTAGGCCTCTGGGCTTTGGGACACTGGTGCCT  
GCTGCTCCCAGCTGGAAAACAAGTTCTATGTCGGTGCAGCATTGTACAGCAGTTGGCTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTACATCTATAGC  
ACCCCTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTACATCCAGTGCAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCACAGTCTCTGCCAGGAATCCC  
GAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCTCTGGGATTC  
ATTCCCTGCTGGAATCTCATGGGATCCTACGGGACTCTACTCACCACGTGCCTGACAG  
CATGAAATTGAGATTGGAGAGGCTCTTACTGGGCAATTATTCTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTCCCTGCTCATCCAGAGAAATCGCTCCA~~ACT~~TACGATGCCTAC  
CAAGCCCAACCTCTGCCACAAGGAGCTCCAAGGCCGGTCAACCTCCAAAGTCAAGAGTGA  
GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAAGAACCAAGGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTAAAAACAGTGGACAGCACCCGAGGGCCACAGGTGAGGGACACTACCACGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCATTGGATTGAGCAAAGGCAGAAATGGG  
GCTAGTGTAAACAGCATGCAGGTGAATTGCCAAGGATGCTGCCATGCCAGCCTCTGTTTCC  
TCACCTTGCTGCTCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCA  
GGACTCAGAGGATCCCTTGCCCTCTGGTTTACCTGGACTCCATCCCCAACCCACTAATCACA  
TCCCAC TGACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAAA~~CT~~GATTGGCCCTGGAACCTCCATCCACTCTTGTATGACTCCACAGTGTCCA  
GACTAATTGTGATGA~~ACT~~GAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

## **FIGURE 80**

MASLGLQLVGYILGLLGLLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSIASSIACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCACACGCGTCCGCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCTTC  
CCCGCGTTCTCTTCCACCTTCTCTTCCACCTAGACCTCCCTGCCCTCCCT  
GCCCACCGCTGCTTCCTGGCCCTCTCGACCCCGCTAGCAGCAGACCTCCCTGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCGTCTCCCTCCGACTCCGCTCCCG  
ACCAGCGGCCTGACCCGGGGAAAGGATGGTCCCGAGGTGAGGGCCTCTCCCTGCTGGGA  
CTCGCGTCTGGTCCCCCTGGACTCCCACGCTCGAGCCGCCAGACATGTTCTGCCTTT  
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTGGAGCCACAAGGCCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCTGGACTCCGGGCCCCACCAAAGTCCCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCCCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
AGATCTCAGTCCCCATGAGCTGTTCCCTCCGCCCTGCCAACCGAGTGTGCTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCCCTCACAACTGCCCGAACCGAGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCCTGCTGCCAACGCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTAGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAG  
AGAGGCCGGCACCCAGCCCCACTGCCCTAGC GCCCTCTGAGCTTCCATGCCACT  
CAGACCCAAGGGAGCAGGCAGCACAACGTCAAGATCGCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGGGAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGC  
CCCTGCCCTGCATCCTATGCACCTGTGAGGATGGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGG  
ACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAAGGTGTCCAAGGCACCGGGCCGGGTC  
CTCGTCCACACATCGGTATCCCAAGCCCAGACAACCTGCCGTGCTTGCCTGGAACACGAGGC  
CTCGGACTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCAAGGCCACAGCAGAATCTTCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTCCAGAAAGAGGCACAGCAGTCCGACTGCTCGTGGCCCCACGAAGGTCACT  
GGAACGTCTCCTAGCCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATATTAATAAA  
TAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
PSRLPNQCVLCSCTEGQIYCGLTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRKGPGTPAPTGLSAPLSFIPRHFRPKAGSTTVKIVLKEKKACVHGGKYS  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLSDQESQEARNPERGTALPTARWPPRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## **FIGURE 83**

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCGCTCACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCAATTAGGCCAGTTCTCTCTCTAATCCATCCGTACACCTCTCGTCA  
TCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTGGTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAG  
GACGCAGCATTCTCTGTTCTGCTCCTAAAGACCAATGCAGAGGCCATGAAAGTGCCTTCAAGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAATGGTGAAGGATTCTATTGGGAGGGCGCATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCTCTATGGGTGCAGGATTAGTCCCAGTCTTAACCAGAAGGCATCTGGAGCT  
ACAGGGTGCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTGTCC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCTGTTCCATGCGGCATGCTCATCTGAGCCGAGGGTGAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAATACTCTGCTGTGGCTA  
TTTTTGGCATTGTTGACTGAAGATTTCTCTCAAATCCAGTGGAAATCCAGGGGAACGGACT  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCACTGGAGGTGACTCTGGATCCAG  
AGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAAGTGTAAACCCATAGAAAAGCTCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTGTCTCCGATCATGGTACTGGTCTCAGACTGAATGGAGAACATTGTATTTC  
ACATTAAATCCCGTTTATCAGGTCTCCCCAGGACCCACCTACAAAATAGGGTCTCTGGACTA  
TGAGTGTGGGACCATCCTCTTCAACATAATGACCAAGTCCCTTATTTATACCCGACATGTCGGTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGCTCTAAATGAGCAAATGGAACCTCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTGGCAAAGGGCTCTCAATCCCAGAGACAAGCAACAG  
TGAGTCCTCTCACAGGCAACCACGCCCTCCCTCCCCAGGGTGAATGTAGGATGAATCACATCCCACAT  
TCTTCTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
GATGAAGGGGACTGCCGTGCCACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGAGGGAAAGAAGG  
CTGACATTACATTAGTTGCTCTCACTCCATGGCTAAGTGTGATCTTGAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGAAGTAAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCTAATGGTTGTCATTATATTACACTTCAGTAAAAAA

## **FIGURE 84**

MALMLSVLSSLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSSVH  
LYRDGKDQPFMQMPOYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELQ  
VSALGSVPPLISITGYVDRDIQLLCQSSGWPRPTAKWKGPGQDLSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRRAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAEQELDWRRKHGQAEQELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRGVCRDDVDRKEYVTLSPDHGYWVRLNGEHLYFT  
LNPRFISVFPPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCTCGGGCCCTGGCACCTCAACCCCAGACATGTGCTGCTGCTGCTGCCCT  
GCTCTGGGGGAGGGAGAGGGCGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTCCGTGA  
CGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCCTACCCCTCGCATGGCTGGATT  
TACCTGGCCCAGTAGTCATGGCTACTGGTCCGGAAAGGGGCAATAACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTGGCAGTGTGGAGGAGACTGGGACCGATTCCACCTCCTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCCGGAGA  
TACTTCTTCGTATGGAGAAAGGAAGTATAAAATGAAATTATAAACATCACCGGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCC  
AGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCTCGGTGCTCACCTCATCCCACA  
GCCCCAGGACCATTGGCACCAGCCTCACCTGTCAGGTGACCTCCCTGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGCTCACCCGCTCAGAACATTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTGGAAATGGCTATCTGTCACTCCCAGAGGGCAGTCT  
GCGCCTGGTCTGTGCAAGTTGATGCAAGCAATCCCCGCCAGGCTGAGCTGAGCTGGAG  
GAGGCCTGACCCCTGTGCCCTCACAGCCCTAAACCCGGGGTGCTGGAGCTGCCCTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCAACCTGCAGAGCTCAGAACCCCTCTCGGTCTCAGCAGGTCTACCT  
GAACGTCCTCCCTGCAGAGCAAAGCCACATCAGGAGTGA  
CTCAGGGGGTGGTCGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCTGTCCCTGCCTCATCTCGGTGACTCAGGGGGTGGTCGGGGAGCTGGAG  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGG  
CATAGAGGATGCAAACGCTGTCAGGGGTTCA  
AGCCTCTCAGGGGCCCTGACTGAACCTGGG  
CAGAAGACAGTCCCCAGACCAGCCTCCCCAG  
CTTCTGCCCGCTCTCA  
GAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTGA  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCC  
TGCAGAGTGA  
GAGGCTGATTCTGAGAATTAA  
CAGCC  
CTCAACGTGATGAGCTATGATA  
AACACTATGAATTATG  
TGCAGAGTGA  
AAAAGCACACAGGCTT  
AGAGTCAAAGTATCT  
AAACCTGAATCC  
CACACTGTGCC  
TCCCTTT  
TTTTTA  
ACTAAAAGACAGACAAATT  
CCTA

## **FIGURE 86**

MLLLLLPLLWGRERAEQTSKLLTMQSSVTVQEGLCVHPCFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVNTALTHRPNILIPGTLESGCPQNLTCSVWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVTLIPIPQPDHGTSLTCQVTFPGASVTTNKTVHLNVSYPQNLTMVFQGDGTSTVLGNSSL  
SLPEGQSLRLVCADVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAEFTCRAQNP  
LGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDTGIE  
DANAVRGSAQGPLTEPWAEDSPPDQPPPASARSSVGEGELOQYASLSFQMVKPWDSRGQEATDTE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGTGAAGGAGCTCTGTAC  
CCAAGGAAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTCTCCGCACTGAGAATGGTTATCTACCAAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGAGTGCACGGTG  
GGCGATCGCTGGTCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGGC  
CAACTACAACACCTTGGATCTGCAGAGGCCAGAGCGATGACTACAAGAACCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTCTCCAGACACTGGACATAATCT  
GTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGCTATGATTTGGCACGCCAGAAAACAGCATCTTATTACTCACCCAT  
GGCAGCGGAATTCACTGCGGATTGTTAGTTCACTGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATAT  
GGAACACTCATGTTGGTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTCTATTCTATCG  
TTGAGAGTTTGTGGAGGGAACCCAGACCTCTCCCAACCAGAGATCCAAAGGATGGAGAA  
CAACTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCS...PLPRSCKEIKDECPSAFDGLYFLRTEN...  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGS...  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWT...DNGPVI...PVYDFGDAQKTASYYSPY...GOREFTAGFVQFRVFN...ERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGY...GTHVGY...SSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## **FIGURE 89**

CTAGATTGTCGGCTTGC~~GGGG~~GACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCCATGGGCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCC~~GGG~~ACAGCAACATA~~CAGG~~CTG  
CCTGCCTCTCACGTTCACCCCCGAGGAGTATGACAAGCAGGACATT~~CAG~~TGGTGGCCGCGCTCT  
CTGTCACCCTGGGCCTTTGCAGTGGAGCTGGCGGTTCTCAGGAGTCTCCATGTTAAC  
AGCACCCAGAGCCTCATCTCCATTGGGCTACTGTAGTGCATCCGTGGCCCTGTCCTTCTCAT  
ATTCGAGC GTTGGGAGTGCACTACGTATTGGTACATTTGTCTTGTCACTGCCCTTCCAGCTG  
TCACTGAAATGGCTTATT~~CGT~~CACCGTCTTGGGCTGAAAAAGAAACCC~~CT~~TGATTACCTTCA  
TGACGGAAC~~CTA~~AGGACGAAGCCTACAGGGCAAGGGCCGCTCGTATTCC~~TG~~GAAGAAGGAAG  
GCATAGGCTTCGGTTTCCCCTCGAAACTGCTTCTGCTGGAGGATATGTGTTGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTAGTGCCTTGTAAATAATGTTTAGTAACA  
TTAAGACTTATACAGTTAGGGACAATTAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFC SALPAVTEMALFV  
TVFGLKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTCGTGTTCCTGGTGCAGGGTAGCCTATCTGGTATCTGTGCCAGGATGATG  
GTCCTCCCGGCTCAGAGGACCCGTAGCGTGATGACCACGAGGGCAGCCCCGGCCGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAACGTCAGTCCCAGGGCATGGCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCCGCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACGCCGAACCACAGCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTACAGGGAAAGATTGTGGACCATGGCAATGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGCTTGCACCCACGACCCAGCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGGCCCTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACATAC  
CATAGTGATAACCCCCACTACCCATCTGGGTGACCCCCGGGCAGGCCACAGAGGCCAGGGC  
TGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAAGGGTTGGCCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATCCAAGTGGGCAGGGCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCAAGTGTGGTCCAACCTGAAGCTGTGGAGTGAAGTACAGGAGCACTGG  
AGGAGGAGTGGCTCTGTGCAGCCTCACAGGGCTTGCACGGGCCACAGAGAGATGCTGGG  
TCCCCGAGGCCTGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAAC  
CCTTGGTTCTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACA  
GCCGTCAACTTAGGATGGATGGCTGAGAGGGCTCCTAGGAGCCAGTCAGCAGGGTGGGGTGG  
GCCAGAGGAGCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCCCTGTCGTGTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTCAAATCCCTCTTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTAACGTAAGACAGGACGATTGTGGCTCCACACTAACGGCCACAGCCCAC  
CGCGTGTGTGTGTCCCTCTCCACCCCAACCCCTGCTGGCTCCTGGAGCATCCATGTCCCG  
GAGAGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCGGGTTCTCCGGATCTGGATGGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGCAGAGCATGTGCTGGATCTGTT  
TGTGTGTCTGTGTGGTGGGGAGGGAGGGAGGGAAAGTCTTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTGGAGCAGGAATAAGCTTGGCCGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVDHGNGTFS  
SVHFQHNATGQGNISISLVPPSKAVEFHQQQIFIEAKASKIFNCRMEWEKVERGRTSLCTHDPA  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCVDNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## **FIGURE 93**

CGGTGGCC**ATG**ACTGC~~GGCC~~GTTCTCGGCTGC~~GC~~CTTCATTGCCTTCGGGCTGCGCTGCC  
CTTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTGTCGCCCTGTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGAGC~~GT~~TGTCTGTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTGAAGAGTATAACCC  
AGGTGAGACAGCACCCTCTATGCGACTGCTGCCATGTTCTGGCTTGGGCTTGGAACATGA  
GTGGAGTATTTCCCTTGTGAATACCC~~T~~ACTGACTCCTGGGGCCAGGCACAGTGGGCATT~~CAT~~  
GGAGATTCTCCTCAATTCTCC~~TT~~TATT~~C~~AGCTTCATGACGCTGGCATTATCTGCTGCATGT  
ATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGAAAAGTGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTCA~~GCCC~~AGACCTTCATAAGTTCTTATTATGGAATAACCTGGCG  
TCAGCATTATAATCCTGGTGC~~T~~CATGGGCACCTGGCATTCTAGCTGC~~GGG~~AGGCAGCTGCC  
AAGCCTGAAACTCTGCCTGCTGCCAAGACAAGAACTTCTTACAACCAGCGCTCCAG**A**  
**A**ACCTCAGGGAAC~~C~~AGCACTCCCAAACCGCAGACTACATCTTAGAGGAAGCACAAC~~T~~GTGCCT  
TTTCTGAAAATCCCTTTCTGGTGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLIFGAFVSVYIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGPVTGVIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAAGGCRSLKLCLLCQDKNFLYNQRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## **FIGURE 95**

AATTTTCACCAGAGTAAACTTGAGAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTGTCTTAGGATCAC  
TCGGTCATTACCACAGCTAAACCTGTTGGACTCCCTCCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTCCTTAAGTCAGTCTGATACCATTAA  
CAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAACCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCTGGGAGGGTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTACACAACTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTGTTCCCGGGAGGCATCCTGCCACCAGTCAGGCAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGTAATCTGCCACCCAGG  
GAACCCCAGCAGGCCGCTCCCAACTCCCAGTGGCACAGATGACGACTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTCAAATTTCAACTAAGCTGCCTCGAATTGGTGATACATGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAATATTCTGAAATTTCAGAAATATGTTATGTAGAGAATCCCAACTTTAAAAAA  
CAATAATTCAATGGATAAAATCTGTCTTGAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAAACATATTGGAAAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## FIGURE 97

## **FIGURE 98**

MVPAWLWLLCVSVQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDGKAT  
EGPFAMDPDSGFLLVTRALDREEQAQEYQLQVTLEMQDGHVLWGPQPVLVHKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
STS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQEYLLQVRAQNSHGEDYAAPPLEHVL  
VMDENDNVPICPPRDPPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVLPPLRAGQNILLVLAMDLAGAEGGSSTCEVEVAVTINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDALEPAFRIMDFAIERGDTEGTFGLDWEPSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLGVPGPGPGATATVTLVERVMPPPQLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWLICIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTLPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPVQRDWRLQTLNGSHAYLTLALHWVEP  
REHIIPVVVSHNAQMWMQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTVAIGIFLI  
LIFTHWTMSRKDKDPQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## FIGURE 99

GGCTGACCGTGTACATTGCCTGGAGGAAGCCTAACGGAAACCCAGGCATCCAGTCCCCACGCCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACAGTAGGAGACCCAGGCTCTGGAAGCACCAGCCTTTA  
TCTCTTCACCTTCAAGTCCCCTTCTCAAGAACCTCTGTCTTGCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTCCAGGCACAAAGAGACAGA**TGAGATGCAGAAAGGAAATG**  
TTCTCCTTATGTTGGTCTACTATTGCATTAGAAGCTGCAACAAATTCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGTCCAG  
TGTGACTCCAGTGGGTTCAGCACAGCCACCATCTCAGGGTCCAGCGTGCACCTCCATGGGTCA  
GCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCCTCAGTGGGCCAGCAGTCACCAACT  
CTGGTCCAGTGTGACCTCCAGTGGAGCCAGCAGTGGGACACTCTGAGTCCAGCAGTCAGTGTCC  
AGTAGGGCCAGCAGTGCACCAACTCTGAGTCTAGCAGACTCTCCAGTGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACCTCCAGTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACA  
CCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTGGGCCAGCAG  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCAGCAGCTCCAGTGGGCC  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACAGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCAGCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACTGAGTCCAGCACAGCAGCTCCAGTGGGCC  
AGTGGGCCAACACAGCCACCAACTCTGAGTCAGTACGACACTCCAGTGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGCAGCACAGCCACCAACTCTGAGTCCAGCACA  
CCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAG  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGAGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACTGAGTCCAGCACAAACCTCCAGTGGGCC  
ACACAGCCACCAACTCTGGGTCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGG  
ATGCACACAACCTCCATAGTCATCTACTGCACTGAGTGGAGGCAAAGCCTGGTGGTCCCTGGT  
GCCGTGGGAAATCTCCATCACCCCTGGCTCGGTTGTGGCGGGCGTGGGCTCTTGTGGC  
TCTTCTCTGTGAGAACAGCCTGCCCAGAACACCTTAAACACAGCTGTCTACCACCC  
CATGGCCTCAACCATGGCCTGGTCCAGGCCCTGGAGGGAAATCATGGAGCCCCACAGGGCAG  
GTGGAGTCTTAACCTGGTCTGGAGGAGACCACTATCATGGAGTGGAGATGGAGGAGGGAGGA  
ACAGCGGGCCCT**TGAGCAGCCCCGGAGACCACTATCATGGAGTGGAGGAGACCTGGCA**  
CCCAAGACCTGGTTCCCTTCATCCAGGAGACCCCTCCAGCTTGTGGAGATCCTGAA  
AATCTGAAGAAGGTATTCTCACCTTCTGCTTTACAGACACTGGAAAGAGAAATACTATAT  
TGCTCATTAGCTAAGAAATAACATCTCATCTAACACACAGCACAAAGAGAAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTGAGATGAACCTAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMOKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATISGS  
SVTSNGSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTTSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGLVPWEIFLITLVVVA  
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGENHGAPHRPRWSPNWFWRPVSSI  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCCTCCCGTACGGGATGAATTAAACGGCGGGTCCGCACGGAGGTGTGACCCCTA  
CGGAGCCCCAGCTTGCCCACGCACCCCCACTCGCGTGCACGGCGGTGCGCTGCTGTACAGGTG  
GGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGTACTCTCTGGAAAGCTGGCAACAAAT  
GGATGATGTGATATATGCATTCCAGGGGAGGGAAATTGTGGTGCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTGAAATCAT  
GGTGTCAGGAAAGGGATTTACTTACTGACTCTGTTGGGAAGCTTTGGAAAGCATT  
TCATGCTGAGTCCCTTTACCTTGATGTTGTAACCCATCTGGTATCGCTGGATCAACAAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTGGTGTAAAAGT  
GATTATAACTGGGGATGCATTGTTCTGGAGAAAGAAGTGTCAATTATCATGAACCACCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCCGTGCGATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGCTCAAAGGTGTTCTGGATTGGTGGCCATGCGAGCTGCTGCCTATAT  
CTTCATTCAAGGAAATGGAAGGATGACAAGAGCCATTGCAAGACATGATTGATTACTTTGTG  
ATATTCAACGAACCACTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTGCTGAAAAAAATGGACTTCAGAAATATGAATATGTTTACATCCAAG  
AACTACAGGCTTACTTGTGGTAGACCGTCAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGGTATCCTCACAAACATTCCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTCACGTCCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCACAAACGGTGGGAAGAGAAGAGAGGCTGCGTCCCTCATCAAG  
GGGAGAAGAATTTATTTACCGGACAGAGTGTCAATTCCACCTTGCAGTCTGAACCTCAGGGTC  
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCCTGTTGAGCCCTGCAATGTCCTACTCAT  
ATATTGTACAGTCTGTTAAGGGTATTATAATCACCATTGAAATCTTGTGCTGCAAGAGA  
GAATATTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTACACAAAACAGCCACAT  
TTAAATTCAAAGAAAATGAGTAAGATTATAAGGTTGCCATGTGAAAACCTAGAGCATATTG  
GAAATGTTCTAAACCTTCAAGCTCAGATGCACTTGCATGACTATGTCGAATATTCTTACT  
GCCATCATTATTGTTAAAGATATTGCACTTAATTGTTGGGAAAAATATTGCTACAATT  
TTAATCTCTGAATGTAATTGATACTGTGTACATAGCAGGGAGTGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTAAACAAATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIFYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLIKEICLKLASKGVPGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDLVHDIRVA  
YPHNIPQSEKHLLQGDFPREIHFHVRYPIDTLPTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCCACGGCTCTGCGCCTGAGACAGCTGGCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCACTGTTCTAGTGTGAGATCAACCCACAGGAATA  
**TCCATGGCTTTGTGCTCATTGGTTCTCAGTTCTACGAGCTGGTGTAGGACAGTGGCAAGT**  
CACTGGACCGGGCAAGTTGTCAAGGCCCTGGTGGGGAGGACGCCGTGTCCTGCTCCCTCT  
TTCCCTGAGACCAGTGCAGAGGCATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGGAAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA  
GTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGCTAAAAAACATCACTCCCTCGG  
ACATCGGCCTGTATGGGTGCTGGTTCAAGTCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCCCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGCCTCAGGCTGGTCCCCCAGCCCACAGCCAAGTGGAAAGGTCACAAGGAC  
AGGATTGTCTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTCCAGCCCTCACCTGGCCTGGCTTCTA  
TTTACTCGGGTTACTCTGTTGCCCCCTGTTGTTGATGGGATGATAATTGTTCTC  
AAATCCAAGGGAAATCAGGGCAACTGGACTGGAGAAGAAAAGCACGGACAGGCAGAAATTGAG  
AGACGCCCGGAAACACGCACTGGAGGTGACCTCTGGATCCAGAGACGGCTACCCGAAGCTCTGC  
TTTCTGATCTGAAACTGTAACCATAGAAAGCTCCCAGGAGGTGCTCACTCTGAGAAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTCTAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAAGAAC  
ATGTGACTTGTCCCCAACATGGGTATTGGTCTCAGACTGACAACAGAACATTGTATTTC  
ACATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTCC  
GGACTATGAGGGTGGGACCATCTCCTTCTCAATACAAATGACCAGTCCCTTATTATACCCCTGC  
TGACATGTCAAGTTGAAGGCTTGTGAGACCCCTATATCAGCATGGATGACGAGGAAAG  
GGGACTCCCATATTCAATGTCCAGTGTCTGGGGAT**TGAGACAGAGAACCCCTGTTAAAGGGC**  
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCC  
CCGGAGCCTGCGCACAGAGTACGCCCTTACTCTCTTAGGGAGCTGAGGTTCTCTGCC  
TGAGGCCCTGCAGCAGGGCAGTCACAGCTTCCAGATGAGGGGGATTGGCCTGACCTGTGGAG  
TCAGAAGGCCATGGCTGCCCTGAAGTGGGAGCGGAATAGACTCACATTAGGTTAGTTGTGAAAA  
CTCCATCCAGCTAACAGCAGTCTGAAGAACAGTCAACACCTCCAGGCTCTCATTTGCTAGTCACGG  
ACAGTGAATTCTGCCCTCACAGGTGAAGATTAAAGAGAACAGAACATGTAATCATGCTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTTTATATTATACATTTCACCCATAAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTATACAAATCACCCATGGAATAGTTATTGAAACACC  
TGCTTGTGAGGCTAAAGAATAAAGAGGGAGTAGGATTTCACTGATTCTATAAGCCAGCAT  
TACCTGATACCAAAACAGGCAAGAAAACAGAAGAAGAGGAAACTACAGGTCCATATCC  
CTCATTAAACACAGACACAAAAATTCTAAATAAAATTAAACTAAACAATATAATTAA  
AAGATGATATATAACTACTCAGTGTGGTTGTCCACAAATGCAGAGTTGGTTAATATTAAAT  
ATCAACCAGTGAATTCAAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPPQPTAKWKGPGQDLSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALCGVVMGMIIIVFFK  
SKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGVYVGVCRDDVDRGKNNVTLSPNNGYWVRLTTTEHLYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTTGAGGGCTAGGAAAAGAG  
TTTGTGGAACCTGGTTATGCCCTCGTCATCTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCAATTATGTGAGATATAATCAAAGAACCTACAATTACTATAGCACATTGTCAATTACAC  
TGACAAACTATATGCTGAGTTGGCAGAGAGGCTCTAACAAATTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTAAAAATGCATTATAAATCTCCATTAGGAAAGAATTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAACATGGAGTGTGGCTCATATGCTGTTGATTGAGATTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTTCAACTTGTACATGAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTTAAATTAAAAAAATCAACAAAGACAGAAACAGACAGCTATCTAAACCAATTGCTGCCA  
ACACGAAGAAGTAAAACCTCTAGGTCAAGACTCAGGATCGTTGGGGACAGAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGTGGAGCAACCTTAATTATGCCACATGGC  
TTGTGAGTGCTGCTCACTGTTACAACATATAAGAACCTGCCCCAGATGGACTGCTTCCCTGGAGTAACA  
ATAAAACCTCGAAAATGAAACGGGTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCTCTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTC  
TCCCTGATGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGACAGGATTGGACACTGAAAAT  
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCTAGAATGTTATGTGCTGGCTCTAGAAGGAAAACAGATGCAT  
GCCAGGGTACTCTGGAGGACCCTGGTTAGTTCAAGCTGGTGTGACTAGAGATATCTGGTACCTTGTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCCAAACAAGCCTGGTGTGACTAGAGTTACGCCCTGGGACTG  
GATTACTCAAAACTGGTATCTAAGAGACAAAGCCTCATGGAACAGATAACATTTTTTGTTTTG  
GGTGTGGAGGCCATTAGAGATACAGAATTGGAGAAGACTTGCACAAACAGCTAGATTGACTGATCTCA  
ATAAAACTGTTGCTTGATGCATGTTCTCCAGCTGTTCCGACGTAAGCATTGCTTGTGCCA  
GATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATTAC  
ATTACAGCCTGTATTCAATTGTTCTCTAGAAGTTGTCAGAAATTGACTGTTGACATAATTGTAAT  
GCATATATACAATTGAAGCACTCCTTCTCAGTCTCAGCTCTCATTCTCAGCAAATATCCATT  
TCAAGGTGCAGAACAAAGGAGTGAAGAAAATATAAGAAGAAAAAAATCCCCTACATTATTGGCACAGAA  
AAAGTATTAGGTGTTCTTAGGAAATTAGAAATGATCATATTGAAAGGTCAAGCAAAGACA  
GCAGAACATCAACTTCACTATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTTATTTCATTCCAAACAACTACTATGATAATTGTGAAGAAGATTCTGTTTTGTGACCT  
ATAATAATTATACAAACTTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATTATTACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAACATCACCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTWHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSRQLESVKNAFYKSPLREFVKSQVIKFSSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKGRL  
RRIIVHEKYKHPHSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAAGCGCTCCAGCTGAAGCCAATGCAGCCCCCTCGGCTCTCCGCGAAGAAGTCCCTG  
CCCCGATGAGCCCCCGCGTCCGCTCCCGACTATCCCCAGGGGGCGTGGGGCACCGGGCCCAGC  
GCCGACGATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTAAAGGATGGGGCTCTCCCTT  
ACGGGGCTCACAA**TG**CCAGAGAAAGATTCCGTGAAGTGTCTCGCCTGCTACGCCCTCAA  
TCTGCTCTTGTTAATGTCATCAGTGTGTTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTAAC TG CAGAACAGGGTAGAGGAAGCAGTCATTTGACTTACTTCT  
GTGGTTCATCCGGTCTGATTGCTGTTGCTGTTCCCTATCATTGTTGGATGTTAGGATATTG  
TGGAACGGTGAAAGAAATCTGTTGCTTCTGCTGGACATATGAACAGGAACCTATGGTCCAGTACAATGGTCA  
GATATGGTCACTTGAAAGCCAGGATGACAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGAATTTCAGAGAGATTAAAGTGTGTTGGAGTAGTATATTCACTGACTGTTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTTAGAGAATTCCAGATGTCACAA  
CAGGCCACCAGGAAGATCTCAGTGACCTTATCAAGAGGGTTGTGGGAAGAAAATGATTCCCT  
TTTGAGAGGAACCAAACAAC TG CAGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCTGGG  
ACAGACCAAATGATGTCCTGAAGAATGACAACCTCAGCACCTGCTGATGTCCTCAGTAGA  
GTTGAAACCAAGCCTGTCAAGAATCTTGAAACACACATCCATGGAACACAGCTTAA  
TACACACTTTGAGATGGAGGAGTT**A**AAAAGAAATGTCAACAGAAGAAAACCACAAACTTGT  
TGTGAATTGGAGTACATACTATGTGTTAGAAATATGTAGAAAATAAAATGTTGCCAAAA  
TAACACCTAACGATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCTGATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTG  
TGTGATGACTTTACTGAACACAGTTATGTTTGAGGCAAGCAGTGGTTGATTGCA  
TCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGGTGA  
CTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTA  
CTCAGCGATCTATTCTCTGATGCTAAATAATTATATCAGAAA  
ACTTAAATGTGATTGGTACTAAATATTCTTACCACTTAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTTAAATCTGATAATT  
TTCAGTCTGATAATGTTAGAATAACCATTATGAAAAGGAAAATTGCTGTT  
ACCTTAAATACCTAACACTAATTGAAAATTACAGTGTGATA  
AGAATGTAGTCTGGCTTTAGGAAGTTAAAGAAAATTGCA  
AAGGACTTGTATGCTGTTCTCCAAATGAAGACTCTTGG  
GCTTATCTTGCCTCTCAGAAAATGCTGAGAATCTTAC  
TAGTGTCTTTCTCAGAAAATGCTGAGAATCTTAC  
CTTGTGTTATTCACTGATTAAATACTGTG  
GAGTATGTTATTGAAATGGAAAAGTC  
TTCTCAGAATATG  
GAAAGAAAATTAAATGTG  
CAATAAATATT  
CTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLNLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMWDPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLSIGVTQILAMILTITLLWALYYDRREPDTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 109**

CCAAGGCCAGAGCTGGACACCTTATCCACTCATCCTCATCCTCTTCCCTGATAAAGCCCCACCAGTGCT  
GATAAAGTCTTCCTCGTGAGGCCTAGAGCCCTTAAAAAAAAGTCTTGAAAGAGAAGGGGACAAGGAACA  
CCAGTATAAGAGGATTTCAGTGTTCCTGGCAGTTGGTCCAGAAGGATGCCTCATTCCCTGCTTCACCTG  
CCTCTCATCACAGGCCACCTCGTGTCAACCGTGGCCCTAGATCCTGTTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACAGTGGATGAGTCAGGTCTCTATGTACAACCATGTAATGGGAG  
TGGTACCACTTCACGGCATGGCGAGATGCCATGCCTACCTTCTGCATACCAAGAAAACACTGTGGAACCCA  
CGCACCTGCTGGCTCAATGGCAGGCCACCCCTAGAAGGCAGGGATTGTGCAACGCCAGGCTGTGCCAGCT  
TCAATGGGAACACTGCTCTGGAACACACACGGTGGAAAGTCAAGGCTTGCCTGGAGGCTACTATGTGTATG  
CTGACCAAGCCCAGCGCTGCTTCCACGCTACTGTGGTCATTATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATAACCAGCGAGTGCACATGGCCTCAGGAACACTGTGCTAGGCCATGACAGGAGACATGCTTG  
ATGAAAATGAATGTGAGCAAACACCGTGGCTGCACTGAGATCTGTGTGAAACCTCAAAACTCCTACCGCTG  
GAGTGTGGGTTGGCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTTGCCTTGGATCTGAGAAAGGCTACAGTGTGAATGTCCCCGGGCCTGGTGTGT  
CTGAGGATAACCACACTTGCAAGTCCCTGTGTTGTGCAATCAAATGCCATTGAAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCCTGGAGCTTCTGACCAACACCTCTGCCAGGGACTGTCCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCATGTGGTAATGACAAGATTGTGGCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCCCGGGAGCAGCAGGGACTCATCATCCGAACCAAGCAGTGTGATCCCC  
ACCTCGCAGTTCCACGCCGTACACCATTCTGAAGGATACGTTCCAACCTCAGAAACTCCCCACTGGAAAT  
CATGAGCCGAAATCATGGGATCTTCCCACTCTGAGATCTTCAAGGACAATGAGTTGAAGAGCCTTAC  
GGGAAGCTCTGCCACCCCAAGCTCGTGAETCCCTACTTGGCATTGAGCCGTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTGCCACCCCACTTCAAGATGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTTCAAGATGACTCGTAAAGCAGTACACATCCCGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGCTTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTGTGGAGTG  
TTGGACGAGCGTCTCCCGTGTGCCACCCAGGGTGTGCCACCGGGAATGGCTGTGGCCAGGAGGAGACTCAGC  
CGGTCTACAGGGCCAGCCTAACAGGCGGCCGATCCGCATCAGTGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTGGAGCTCTCCCCCACCAGGCTCTAAAGAACATCTGCCAACAGC  
TGGGTCAGACTCACACTGTGAGTCAGACTCCACGACCAACTCACTCTGATTCTGGTCATTCAAGTGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCTGGGTTTCATCTTCTAGGGTTGAAAACAACTAAACTGTCCA  
CCCAGAAAGACACTACCCCAATTCCCTCAATTCTTCCACTAAATACCTCGTGTATGGTCAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTCAAGTTACAAACCCATGAAAATTAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTAAATATGTAATATAGTTACCTGAAATTCAATTCAAATGCAAGACTAA  
TTATAGGAATTGGAAGTGTATCAATAAACAGTATATAATT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPEHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYYVRLTKPSVCFHV  
YCGHFYDICDEDCHGCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDVEGCHNNNGCASHCLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFFLTNTSCRGVSNGTHVNILFSLKTCGTVVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEPPYREALPTLKLRSLSYFGIEPVVHV  
SGLESLVESCFAATPTSKIDEVLKYLYIRDGCVSDDSVKQYTSRDHLAKHFQPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQQQLTGGLPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACACTCGG  
GCCCTCCAGCCAGTGTGACCAGGGACTTCTGACCTGCTGGCAGCCAGGACCTGTGTGGGAGGCC  
CCTGCTGCCCTGGGGTACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCGTATCCCC  
ATGGAGACCTTCAGAAAGTGGGATCCCATCATAGCACTACTGAGCCTGGCAGGTATCATCATTGT  
GGTTGTCCATCAAGGTATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCTTGGGGAGGACGAGGAGCACTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCGCCTCTCCAAGGACCGATCACACTGCAAGGTGCTGGACTCGGCCAC  
AGGGAACCTGGTCTCTGCCTGTTGACAACACTCAGAGCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGCCAGACCAAGGATCTGGATGTTGAAATCACAGAAAAGCCAG  
GAGCTTCGATCGGAAACTCAAGTGGCCCTGTCCTCAGGCTCCCTGGTCTCCCTGCACGTCTGCC  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGTGGGAGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGCCTCACGGCA  
GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCCACACTCACTTCAGGCACAGTCAGGCCATCTGTCTGCCCTTCTT  
GATGAGGAGCTCACTCCAGGCCACCCACTCTGGATCATTGGATGGGCTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCAGGCTATTGACACGACACCGGTGCAATGCAAGCAG  
ACCAGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACAGTGGCATGTGGTGGGATCGTTACGTGGGCTATGG  
CTGGGGGGCCCGAGCACCCAGGGAGTACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGTGAGCTGTAATGCTGCTGCCCTTGCAGTGCTGGAGCCCTCCCTGCCCTGCCACCT  
GGGATCCCCAAAGTCAGACACAGCAAGACTCCCTGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTGGAGCAGCAAAGGCCCTCAATTCTGTAAGAGACCCCTCGCAGGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCTAGCTCGGCCACACTGGTGTCCAGCATCCAGGGAGAGACACAGCCCACTGAAACAAGGTCT  
CAGGGTATTGCTAAGCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGGCCCTGCCGTCTCACCCATCCCCAA  
GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCTGGCAAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLKVILDKYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDLSATGNWFSACFDN  
FTEALAAETACRQMGYSRAVEIGPDQDLDVVETENSQELRMNRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGGEAASVDSWPWQVSIQYDKQHVC CGSILDPHWLTAAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLA VAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPPFDEELTPATPLWIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDT CQGDGGPLMYQS  
DQWHVVGIVSWG YGC GGPSTPGVYTKV SAYLNWIYNVWK AEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

### **FIGURE 113**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAACTGCTAGGATTCTGACTATGCCTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
TGTCCCCCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCACTGTGGCT  
GGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCGTCCCCTGAAG  
CCGGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCTCACCAACTGTCTACGTCT  
GGAGGCCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTGGTAGCTGCGGTTCAAGGTGGC  
CTTGCCCTGGCGTAGAAGGGATTGACAAGCCGAAGATTTCATAGGCATGGCTCCACTGCC  
AGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGCCAGGACGGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCGCCATCTAACCTTTCATGTCCTGCACATCACCTG  
ATCCATGGGCTAACCTGAACCTGTCCCAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGCTGCTTAGACCACCTGGTTATGTGACAGGACTTGCAATTCTCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAAGGAACCTGTGCCAAATTATGGGTAGAAAAGATG  
GAGGTGTTGGTTATCACAAGGCATCGAGTCTCTGCATTCACTGGACATGTGGGGAAAGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGAT  
CCACGTACCAAGCTGCTGAAGGGCAACTGCAGGCCATGCTCTCATCAGCCAGGCCAGCAGCCAAA  
TCTGCGATCACCAGCCAGGGCAGCCGTCTGGAAAGGAGCAAGCAAAGTGACCAATTCTCTCCC  
CTCCTCCCTCTGAGAGGCCCTCTATGTCCCTACTAAAGCCACCAAGAACATAGCTGACAGG  
GGCTAACGGCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCATGAGAGCTGATCAGAAGGGCTGCT  
GTGCGAACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTGGTT  
CAAATGATCTCAAGGGCCCTTATACCCAGGAGACTTGATTTGAATTGAAACCCCAAATCCA  
AACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGTGTGGCTGTAATGCCAACAT  
TTTGGGAGGCCAGGGCGGTAGATCACCTGAGGTCAAGGACTGAGGCTGGCCATGGCCAAACATGG  
TGAAACCCCTGTCTACTAAAAAATACAAAAAAACTAGCCAGGCTGGTGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAAACCTGGAGGTGAAGGAGGCTGAGACA  
GGAGAACATTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATT  
TGGTTATTGTAA

## **FIGURE 114**

MLWWLVLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLAELTRAVQVAEPLGSCGFQGGPCPGRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTGTGGACTGGTGTGTTGCTGGCCCTAACTCTAATTGTCT  
GTTTGCCCCAGCAAGCACCTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTACATGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAACGGAAATGGCACTGATGAAACATTGAAAGTGCACGACTTAAAAACGGATACACTGG  
CATCTACTCGTGGGTCTCAAAATGTTTATCAAACACTCAGATTAAGTGAATTCTGAATT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCAACTTCTTGAACAGTCAGTG  
ATTGGGTCCCAGCAGAAAGCCTATTGAAACCCGAGATTCTTCTTAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCACTCTAATATCAGTTCTGAGTTACAAG  
ACTTTGAGGAGGGAGGAGAAGATCTTCACTTCCCTGCCAACGAAAAAAAGGGATTGAACAAAAT  
GAACAGTGGTGGTCCCTCAAGTAGAAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTCCAATAATGACTATACTGAAATGAAATTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGATTACTGCCGTCAGGCAACCGCTATTGCCGCCGCTGTGAACCTTACTA  
GGCTACTACCCATATCCACTGCTACCAAGGAGGACGAGTCATCTGCGTGTACATGCCCTG  
TAACTGGTGGTGGCCCGCATGCTGGGAGGGCTTAATAGGAGGTTGAGCTAAATGCTTAAAC  
TGCTGGCAACATATAATAATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCT  
GGTAGGCCAGCTCTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAATAAAACTCTACA  
TTATCACCAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLLIVLFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHF PAN EKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMED  
ERGYCCIYCRRGNRYCRRVCEPLLGGYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTAGCTTCACACCTCGCAGCAGGAGGGCGGCAGCTTCTGCAGGGCA  
GGCGGGCGGCCAGGATCATGTCCACCACATGCCAAGTGGTGGCGTCCCTCCTGTCCATCCTGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTGGAGGAGCTGCGTGAGGCAGAGTCAGGCTTCACCGAATGCAGGCC  
TATTTACCATCCTGGACTTCAGCCATGCTGCAGGCAGTGCAGCCCTGATGATGTAGGCATCGCCT  
GGGTGCCATTGGCCTCTGGTATCCATCTTGGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCGGGATCATGTTCATTGTCAGGTCTTGTCAGGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAATTCTGGATGTCCACAGTAACATGTACACCGCATGGTGG  
GATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCAGGCTGTTCTGGCTGGCTGGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGCTGGCACCAAGAAGAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCCACAGTGGTGCCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAAACAAGAAGATATACTGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGCACTATGTGTAATGCTCTAACAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCA  
CCCCAAAAACAAGGAGATCCCACATCTAGATTCTCTGCTTTGACTCACAGCTGAAAGTTAGAAAGCCT  
CGATTTCATCTTGGAGAGGCCAATGGTCTTAGCCTCAGTCTGTCTCAAATATTCCACCATAAAACA  
GCTGAGTTATTATGAATTAGAGGTATAGCTCACATTCAATCCTCTATTCTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGTTTAATCTCTCTCACATTGATGATTAGACAGACTCCCCCTC  
TTCCCTCTAGTCATAAAACCCATTGATGATCTATTCCAGCTTATCCCCAACAAAACCTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTCTGCTGTTGAATTGCTCTCCCCACCCCAACTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTGTAATCTCCAGGCCATGATCTGGTTTCTT  
ACACTGTGATCTTAAAGTTACCAACCAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTGCTG  
TTGACATCTCTTATTACAGCAACACCATTCTAGAGTTCTGAGCTCCACTGGAGTCTCTTCTGT  
CGCGGGTCAGAAATTGCTCTAGATGAATGAGAAAATTATTCTTAATTAAAGTCCTAAATATAAGTTAA  
AATAAAATAATGTTAGAATGATACTATCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAAATAATTGCTTGCATTGTCATATGGTACTTTGTAAGTCATGCTTAAGTACAATTCC  
ATGAAAAGCTCACACCTGTAATCTGACTTTGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGCTCACAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATACACCTGTAAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGGCCAGGGAGGT  
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAA  
AATAAAATAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

## **FIGURE 118**

MSTTCQVVAFLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKA  
STGFGSNTKNKKIYDGGARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCGGAGTCC  
AGCTGGCTAAACATCCCAGAGGATAATGGCAACCCATGCCTAGAAATCGCTGGCTGTTCTTG  
GTGGTGTGGAATGGTGGCACAGTGGCTGTCACTGTCACTGCCTCAGTGGAGAGTGTGCGCCTTCATT  
GAAAACAACATCGTGGTTTGAAAACCTCTGGAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCACAAATCTATGATCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGGCCAGAG  
GACTGATGTGTGCTGCTCCGTGATGTCCTCTGGCTTCATGATGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCAT  
CATCACGGGCATGGTGGCTCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCCTGATTGTTGGAGGAGCTCTGTTCTGCGTTTTGTTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTCCATCGCACACCCAAAAAGTTATCACACCGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTTAGTTGTATGTTTTTAACTTACTATAAACCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAATGGACCCCCAAGAAAACCTTGATTTACTGTTCTTAACGCCT  
AATCTTAATTACAGGAACTGTGCATCAGCTATTATGATTCTATAAGCTATTCAGCAGAATGAGATA  
TTAACCCAATGCTTGATTGTTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCATA  
CTCTTTTATCAATTACTTCAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATCTCACATAGAGACATGCTTATATGGT  
TTTATTAAATGAAATGCCAGTCCATTACACTGAATAAAATAGAAACTCAACTATTGCTTTCAGGGAA  
ATCATGGATAGGGTGAAGAAGGTTACTATTAAATTGTTAAAACAGCTIAGGGATTATGTCTCCA  
TTTATAATGAAGATTAAATGAAGGCTTAATCAGCATTGTAAGAAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCCTAACATTCTTATCCTCTCCAGAGGCTTTTT  
CTTGTGTATTAAATTAAACATTAAACGAGATAATTGTCAGGCTTGCATTCAAACGTCT  
TTCCAGGGCTATACTCAGAAGAAGATAAAAGTGTGATCTAAGAAAAGTGTGTTAGGAAAGTG  
AAAATTTTTGTTTGATTGAAGAAGAATGATGCATTGACAAGAAATCATATATGTATGGAT  
ATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATCAATAAATAAAAGAGCAGAAAATA  
TGTCTGGTTTCATTGCTTACCAAAAAACACAACAAAAAAAGTGTCTTGTGAGAAACTCACCT  
GCTCCTATGTGGTACCTGAGTCACATTGTCATTGTTCTGTGAAAATAATTCTTCTGTA  
CCATTCTGTTAGTTACTAAATCTGAAACTGTATTGTTCTGTTATTCAAATTGATGAA  
ACTGACAATCCAATTGAAAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTATTAATAAAATTGTACATTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRGTGDNEVKAHILLTAGIIFIITG  
MVVLIPSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAGGCATTGATGCAGCCTGCCGCGCCTCGGAGCGCGCGAG  
CCAGACGCTGACCACGTTCCCTCCCTCGGTCTCCGCCCTCCAGCTCCCGCTGCCGGCAGCC  
GGGAGCCATGCACCCCAGGGCCCCGCCCTCCCGCAGCGGCTCCGCGGCCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCGCCGTGAGCGCCTCTGAGATCCCAAGGGGAAGCAAAGGCCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGC  
TGGTCGAGACGGGAGCCCTGGGCCAATGTTATTCCGGTACACCTGGATCCCAGGTGGGATG  
GATTCAAAGGAGAAAAGGGGGAAATGTCGAGGGAAAGCTTGAGGGAGTCTGGACACCCAACATAC  
AAGCAGTGTTCATGGAGTTCATTAATTGGCATAGATCTGGAAAATTGCGGAGTGTACATT  
TACAAAGATGCGTCAAATAGTGTCTAAGAGTTGTCAGTGGCTCACTTCGGCTAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTCAATTCAATGGAGCTGAATGTTCAAGGACCTCTCCC  
ATTGAAGCTATAATTATTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAAATTATCG  
CACTTCTCTGTGGAAGGACTTGTGAAGGAATTGGTGGATTAGTGGATGTTGCTATCTGG  
TTGGCACTGTTAGATTACCCAAAAGGAGATGCTTCACTGGATGGAATTCAAGTCTCGCATC  
ATTATTGAAGAACTACCAAATAAATGCTTAATTTCATTGCTACCTCTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTTAAATAAGTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTACAGACCAAAAGTGTGATTTCACACTGTTTAAATCTAGCATTATTCAATTG  
CTTCAATCAAAAGGGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATT  
CTCTCAACCTATAATTGGAATATTGTTGGTCTTTGTTCTCTTAGTATAGCATTAA  
AAAAAAATATAAAAGCTACCAATTTGTACAATTGTAATGTTAAGAATTTTTTATATCTGT  
TAAATAAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFGSLLRKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDVIAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGGTACGGGCCTCCTGCCCTGGGCTCCAACGCAGCTGTGGCTGAA  
CTGGGTGCTCATCACGGGAAC TGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCCTGGAAGAATACATCATGTTTCGATAAGAAGAAAATTGTTAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCACCCCCCAAAAAACTGTAAGAGTGCAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTGATTTGCTGCGAATGCCGTGTTGGGATTATTGTTCTGGAG  
TGGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCAAAGGGTCCAATT  
TCTTCTGGGTGTCAGCGAGCCTGACTCACAGTGACGTGACAGGGCTGTCATGCAACTG  
GCCCTAAGCCAAGCAAAGACCTAACGGACGACCTTGAACAATACAAAGGATGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTAGCCCCACTGCTTACTGACAATG  
CTTTCTCTGCCAACGAGGATGCCCTAACGGCTGTAGGTGTGAAGGCAAATGGTATATTGTA  
ATCTCAGAAATTACAGGAGATACCCCTAACGTTAGTATCTGCTGGTTAGGTTGCTTCCCTCGCT  
ATAACAGCCTCAAAAACCTAACGTTAGTATAATCAATTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATTAGACGAAAATGCTTTAATGGAATACGCAACTCAAAGA  
GCTGATTCTTAGTCCAATAGAATCTCTATTCTTAACAATACCTTCAGACCTGTGACAATT  
TACGGAACCTGGATCTGCCCTATAATCAGCTGCATTCTGGGATCTGAACAGTTGGGGCTTG  
CGGAAGCTGCTGAGTTACATTACGGCTAACCTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGCCAACCTGGAACCTTGGACCTGGGATATAACGGATCCGAAGTTAGCCAGGAATG  
TCTTGCTGGCATGACTAACAGAACCTCACCTGGAGCACAATCAATTCCAAGCTCAAC  
CTGGCCCTTTCCAAGGTTGGCAGCCTCAGAACCTTACTTGCACTGGAATAAAATCAGTGT  
CATAGGACAGACCATGTCCTGGACCTGGAGCTCTAACAAAGGCTGATTATCAGGAATGAGA  
TCGAAGCTTCAGTGGACCCAGTTTCCAGTGTGTCCGAATCTGCAGCGCTAACCTGGAT  
TCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAG  
TCTTGCTGGGAATATGGGAATGCAAGCAGAAATATTGCTCCCTGTAAACTGGCTAAAAGTT  
TTAAAGGTCAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGACTGCAAGGGAGTAAATG  
ATCGATGCAAGAAACTACAGCATCTGGGCAAAGACTACAGAGAGGTTGATCTGGCAG  
GGCTCTCCCAAAGCCGACGTTAACGCCCAGAGGCCAGAGACCGATGTCAGCGCAGCACATCT  
TGCCCCCGAGGTGGAGCCACAGAGGCCAGAGACCGATGTCAGCGCAGCACATCT  
TTCCATAAAAATCATCGGGGAGCGTGGCCTTCTGTCCGTGTCATCTGCTGGTTAT  
CTACGTGTCATGGAGCGGCTACCTGCGAGCATGAAGCAGCTGCGAGCGCTCCCTCATGCGAA  
GGCACAGGAAAAAGAAAAGACAGTCCCCTAACGAAATGACTCCCAGCAGGAAATTATGTA  
GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGATAAAAAGAGCTTAAAAGCT  
GGGAAATAAGTGGTCTTATTGAACTCTGGTGAATCAAGGGAAACGCGATGCCCCCCCCTCCCC  
TTCCCTCTCCCTCACTTGGTGGCAAGATCCTCTGTGCGTTAGTGCATTCAATAACT  
GGTCATTTCTCTCATACATAATCAACCCATTGAAATTAAATACCAACATGTAAGGCTT  
GAACTCGGTTAATATAATACATTGTATAAGACCCCTTACTGATTCCATTATGCGCATTT  
GTTTAAGATAAAACTCTTCTAGGTAAAAAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLMLSSAERGCPKGCRCEGKMYCESQKLQEIPSSISAGCLG  
LSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKELHLEHNQFSKLNLALFPRLVSLQNLQWNKISVIGQTMSTWSSLQRLDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLFIGQEILDWSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELOQGVNVIDAVKNYSICGKSTTERFDLARALPKTFKPKLPRKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVLIVYVSWKRYPASMKQIQR  
SLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGBTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTCGCTACTGCTGAATGTCCGTCCCGGAGGAGGGAGGGCTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCAGCAAATTCTACTGTCCGGCTGC~~CG~~GGCTACCGTGGCCAGCT  
AGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAATGCAAGGAGAAGCAGCTTGTCTC  
GGTGGGAGACGGTGAAGAGAAATCTGCCCTATAGGGGAATGGTGCACAGCCCTAGGATC  
ATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCATTACAGACACGTAGT  
GTATTCTGGAGGTCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTATTGGCCAGTT  
TTAGCCAATCCAACTGACCTAGTGAAGGTTCAGATGCAAATGGAAGGAAAAGGAACTGGAAGG  
AAAACCATTGCGATTCTGTGGTGTACATCATGCATTGCAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTGGCAGGCTGGTACCCAAATATACAAAGAGCAGCACTGGTGAATATGGGAGATT  
ACCACTTATGATAACAGTGAAACACTACTTGGTATTGAAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTATCAAGTTATGTTCTGGACTGGTAGCTCTATTCTGGAACACCAGCCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAACAGGAAGGGACTTTGATAAAATCATCG  
ACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAAGGCTTTACC  
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIEEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIKSrimnQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRTPWMSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 127**

CGCGGATCGGACCAAGCAGGTGGCGCGCGCAGGAGAGCGGCCGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCAGGGCGTGGGCCATGGCCAGGCCGGCATGG  
AGCGGTGGCGCACCGCTGGCCTGGTACGGGGCCTCGGGGGCATCGGCAGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCGCCGCACTGTGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTCAGGCTACCCCAGGACTTTGATCCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCGGCCTGACACCCCTGCTCTCAGGCAGCACCCAGTGGTTGGAA  
GGACATGTTCAATGTAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGCACATCATTAACATCAATAGCATGTCGGCCACCGAGTGTAA  
CCCCTGTCGTGACCCACTTCTATAGGCCACCAAGTATGCCGTACTGCCGTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGGCCACGTGCATCTCCAGGTGTGGTGG  
AGACACAATTGCCCTCAAACCTCCACGACAAGGACCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCGAGGATGTGGCGAGGCTGTATCTACGTCCTCAGCACCCCCGACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACACTGTGGAGCTCC  
TCCTTCCTCCCCACCCCTCATGGCTGCCCTGCCTCTGGATTTAGGTGTTGATTCTGGAT  
CACGGGATAACCACTCCGTCCACACCCCGACCAGGGCTAGAAAATTGTTGAGATTTTATA  
TCATCTGTCAAATTGCTTCAGTTGTAATGTGAAAAATGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGCCCTGGCACTTGGCTTGTCTGCTCTCAGTG  
TCTTCCTTGACATGGAAAGGAGTTGTGCCAAAATCCCCATCTTGCACCTCAACGTCTG  
TGGCTCAGGGCTGGGCTGGCAGAGGGAGGCCTCACCTATATCTGTGTTGTTACCGGGCTCC  
AGACTTCCCTCTGCCTGCCCACTGCACCCCTCTCCCCCTATCTATCTCCTCTGGCTCCCC  
AGCCCAGTCTGGCTTGTCCCCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCTGGCCAGTGGATTGATGGTGCATTAAAAAGAAAAATCGCAACCAA  
AAAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLPLSVTHFYSATKYAVTALTEGLRQEELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMCKLPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCCTTGACTGCAGGCGTCAGGTGCAGAGTCAGTGCCCCGGAGC  
ACCTCCCTCCCAGGGCAGTCTGCTCAGAGGGCCTCGGCCAGAATTCCAGTTCTGGTTCATGC  
CAGCCTGAAAAGGCCATGGAACTTGGGTGAATCACCGATGCCATTAAAGAGGGTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTCTGCGCTGTTCATTCAGTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAAATGAGGAAACTGAGAAAATTAATTCTCATGTATTTCTCATTATTAA  
TTAATTAATTTAACTGATAGTTGACATATTGGGGTACATGTGATATTGGATACATGTATACAA  
TATATAATGATCAAATCAGGGTACTGGATATCCATCACATCAAACATTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCAAAGTAGCTGGACTACAGGCAT  
GCACCACAATGCCCAACTATTTGATTTAGTAGAGACGGGTTTGCCATGTTGCCAGG  
CTGGCCTTGAACTCCTGGCCTCAAACAACCATTGCCTCGGCCTCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCTAAACATTTATCTTGTGTTGGAAACTTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAAACACTGGACTTCTCCCTCT  
ATCTAACTGTATATTGTACCAGTTAACCAACCGTACTTCATCCCACCTCTCTATCCTTCCC  
AACCTGTATCACCTCATTCTACTCTCACCTCCATGAGATCCACTTTTAGCTCCACATGTG  
AGTAAGAAAATGCAATATTGTCTTCTGTGCTGGCTTATTCACTTAACATAATGACTCCTG  
TTCCCATCCATGTTGCTGCAAATGACAGGATTCGTCTTAATTCAATTAACATAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRSVAREHLPSPRGSSLRGPRPRIPVLVSCQPV  
KGHGTLGESPMFKRVFCQDGTVRSFCVCAVFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTGTATAAAGACCTAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCCATCGGGACTAAAATTGGGCTGTCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTCGCTCGCATGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACTCTACCTCAGAACAAACAAATAATGCTGGATTCTTCAGAT  
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACTACCTACACAAACAGTTAGATGAATTCTACCAACCT  
CCCCAAAGTATGTAAGAGTACATTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGGAAGAATTACATTAGATGACAACACTGTCCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCGACTGCTTTCTGTCCTCGTAATCACCTAGCACAATTCCCTGGGTT  
GCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCATCTCTCAAG  
GTCTCACTAGTCTAAACGCTGGTCTAGATGAAACACTGTCCTGCAGTTAGGTGACAAGATT  
TTCTTCAACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGCACAGTAAACCT  
TCCAGGGACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAACGGGTGCCCTAAATGCTTTT  
CTTATCTAAGGCAGCTATCGACTGGATATGTCATAAAACCTAAGTAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACGATTCTCGAACAACTCCCTGGTATTGCGGGTGCAAGATGAAATG  
GGTACGTGACTGGTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGTCATGTGCCAAGCCCCAGAAA  
AGGTTGGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACCTGCAAAACACAGTGTATCTGCCAAGGACAGTGGCCAGCTCAGTGAC  
CAAACAGCCAGATATTAAGAACCCAAAGCTCAACTAGGATCAACAAACACAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTCTGTCACCTCTGATACCATTCTATCTGGAAACTGCTTACCTATG  
ACTGTTGAGACTCAGCTGGTAAACTGGGCAATGCCCGCATTTGATCTATAACAGAAACAATTG  
AACAGGGGAAACGCAACCTCTACCTATTGATGAAACTCCTGTTGATTGAGACTGAAACTGCAACCCCT  
CCATGGAAACAGCAACCTCTACCTATTGATGAAACTCCTGTTGATTGAGACTGAAACTGCAACCCCT  
CGAATGTACAACCCCTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTAC  
TTGGCTGCCATCATTGGTGGGCTGTGGCCCTGGTTACCATGGCCCTTCTGCTTAGTGTGTTGGTATG  
TTCATAGGAATGGATCGCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTATCCTGGAAATCAGGGAAACCTTCTTCAAGATGTTACCAAT  
AAGCAATGAACCCATCTGAAGGAGGAGTTGTAATACACCCATATTCTCTCAATGGAATGAATCTGT  
ACAAAAAACAAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTGGGTTTTAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHQENNIRTITYDSSLKIPYL  
EELHLDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLS TIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAA PVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWVDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQTTAIPNTVPAQGQWPAPVTKQPD  
IKNPKLTKDQQTTGSPSRKTITITVKS VTS DTIHISWKLALPMTALRLS WLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKCMVPMETS NLYLFDETPVC IETETAPLRMYNPTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRKDDYAEAGTKKD NS  
ILEIRETSFQMLPISNEPISKEE FVIHTIFPPNGMNLYKNNHSESSSNRSYR DSGIPDSDHS HS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCCCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGGCG  
TGCAGAGGCAGTCTGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGCTGCTGCTCTGCTTAAGTACAGCAGTGCACCCAGCTGTGGT  
CCTCCTCACTGCCCTGGCTGGACACTGCTGAAAGTAAAGCCACCATGAGACCTGATCCTGTCT  
GCGCTGGAGAGAGGCCACCGTCTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCGAGTGTGGAAGAGCAGCTAAAAGTGTCCGGAGAAGTGGGCCAGGAGCCCCCTGC  
TGCAGCCGCTGAGCCTGCGCGTGGGATGCTGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCAAAGTACCTAACAGAGAGTCCAGCTGACCCCTCCAGCCCCG  
GTTTGAAAGCTCCCACATGCCCTGGATCCACACTGATGCCCTTGGTGTACCCACGTTGGG  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCCTGCCCCACCAACTGCTCTTCTCTGGGCCAGAATGAGGGATGCACACAGG  
GACCACCTCAAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATGGATAACGCCCTACCCGGACATCTTCATGGAAAACATCATGTTCTG  
TGGAAATGGGGGGCTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTCGAGGGAGGTGAAGAGGCCAGAAAAACAATTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTGGCTCACTGCAACCTTGCCTCTGGTTCAAGC  
AATTCTTGCCTCATCTCCCAGTAGCTGGACTACAGGAGCGTGCACCATACCTGGCTAAT  
TTTATATTTTTAGTAGAGACAGGGTTCATCATGTTGCTCATGCTGGTCTCGAACACTCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTCAAAGAGACTGTGTTGAATAAAGGGCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCCCTAGATGGCTGCTCTCCACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTCCTATACTCCTGGCAGAAATACCCCCCAGCAAAACAGAGAGGCCACACCCATCCACACCG  
CCACCAAGCAGCCGCTGAGACGGACGGTCCATGCCAGCTGCCCTGGAGGAGGAACAGACCC  
TTAGTCCTCATCCCTAGATCCTGGAGGGCACGGATCACATCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTCAACTGCAACTGAACTGAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSGLARAQGAERVTSSERPMASLGLLLLLTLAPPLWSSSLPGLD  
TAESKATIADLILSALERATVFLERQLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCAANMMDLNRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFQFSCLILP  
SSWDYRSVPYLANFYIFLVETGFHHVAHAGLELLISRDPPPTSGSQVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTCCCGCTGCTGCTG  
CTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTCAAGATTGAGGGCGTGAGTTGTCAGGGGTGAAGC  
CTCAGGACTGGATCTCGCGGCCGAGTGCCTGGTAGACGGAGAACGACGTCGGTTCTTAAG  
ACAGATGGGAGTTTGTGGTTCATGATATACTCTGGATCTTATGAGTTGAAAGTTGATCTCC  
AGCTTACAGATTTGATCCCGTCAGTGGATATCACTTCGAAAGAAAAATGAGAGCAAGATAG  
TGAATTACATCAAACATCAGAGGTTGTCAGACTGCCATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAAGGAATCGTGGGGCTGGACAGACTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTCCTTATTGATATTGTGCTCTGCCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGAAATGGAGCAGTCATGAATATGCTGAATTCCAACCAGTGGCTGAT  
GTTTCTGAGTTCATGACAAGACTCTCTCTCAAATCATCTGGCAAATCTAGCAGCGCAGCAG  
TAAAACAGGCAAAGTGGGCTGGCAAAGGGAGGTAGTCAGGCCGTCAGAGCTGGCATTGCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAATT  
GAGTCATCCCACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTGTACTTGGTACACGAGAAAACCCAGCTTCATCTTGCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAAATTACAGTGTCTATAGAAAATGCCATTAATAATTAT  
ATGAACTACTATACTATTATGTATATTAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSEVPGAAEGSGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMSSGPPSYFIKRESWGWTDFLMNPVMMMVLPLLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGT GAGCTACGTTGGCTTCTGAAAGGGGAGGCATATTCGCTCAATTCCCCAAACAA  
GTTTGACATTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGCACTAACGGCGAGCCAGGATGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTCTCACGGGAGGCTGGCAGT  
TTTCTTACTCCTGTTGCTCCAGATTCAGGCCTAAGATGAAAGCCTAGTCTTGCTTCAGC  
CTTCTCTGCTGCGTTTATCTCTATGGACTCCTTCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTCTGAGATA CGGGGCAGTG  
TGCAAGCCAAGATGAAACATTGACATCAGAAATCTTAAGGAGGACTGAGTCTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCCTGCGCCATTGCTAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAAGATCAGCAGCCTCGCCAATTCTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTPGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTGACTGCACTTAAAAGCTGGAACCTCAGGCAGCAGTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTCAATACCTGAGAGGAGCATGACCCAA  
ACCACCATCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTG  
CTTCCTGCTGATGATTGCTTTATGCATCCCCATCTAATTGAGACCATCTGTATAAGATTT  
TGTAATATCTTCTGCTATTGGATATATTATTTAGTTAATATTTATTTATTTGCTATT  
ATGTATTTATTTTACTTGGACATGAAACTTAAAAAAATTCAACAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAAAAACCTTGTAAATTCTAGAAGAGTGG  
CTAGGGGGTTATTCACTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGATGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCACCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG  
CCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTTCTTGCTACCAAAAAAAA  
AAAAAAAAAAA

## **FIGURE 138**

MRQFPKTSFDISPMSFSIYSLQVPAVGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLRHLLRLYLDdrvFKNYQTPDHYTLRKIS  
SLANSFLTICKDLRLSHAHMTCHC GEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCAGGTGGGTCGGTCCGCATCCAGCC  
TAGCGTGTCCACGATGCGGCTGGGCTCCGGACTTCGTACCTGTGCGTAGCGATCGAGGTGC  
TAGGGATCGCGGCTTCCTCGGGATTCTCCCGCTCCCGTGGAGCCAGTTCTAAGTGGACCACGCTGCC  
CACGGAGCGGAGGCCCGAGCGCCGAACCCCTGGCTGGAGCCAGTTCTAAGTGGACCACGCTGCC  
ACCACCTCTTCAGTAAAGTTGTTATGTCAGTAAAGTGGAGAGATGATTGTGTTTG  
GGTCAAAGGGTGTGAAATTATGGCCACACAACCTAACCTTGAGAGATGAAACCTGGGTAAATTAA  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCATCAAGGCATTGACGGGGAG  
CCTTCCTGGCTTGTGACGTCATCAGGAACCTCAATTCTCTGCACTGCTGGAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAAAGAATAGTCTTTATGGAGATGAAACCTGGGTAAATTAA  
TTCCCAAAGCATTGTGGAATATGATGGACAAACCTCATTTCTGTCAGATTACACAGAGGT  
GGATAATAATGTACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGACATATTAATCC  
TCCACTACCTGGGCTGGACCACATTGCCACATTCAAGGGCCAACAGCCCCCTGATGGCAG  
AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCACTGCAAGGAGAGAGA  
GACGCCCTTACCCATTGCTGGTTCTTGTGGTGCACATGGCATGTCAGTAAACAGGAAGTCACG  
GGGCCTCCTCCACCGAGGGAGGTGAATACACCTCTGATTTAATCAGTTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAAGCACGTCAAAGCACGTCATAGACGGATGTGGCTGCACACTGGCAGTAGC  
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTCACATTGAATACAGTGCAGCTAGTAAACTGTTGCAAGAG  
AATGTGCCGTATGAAAAAGATCCTGGTTGAGCAGTTAAAGTCAAGAAAGATTGCATGG  
GAACGTGATCAGACTGTACTTGGAGGAAAAGCATTCAAGACGCTCTATTCAACCTGGGCTCCAAGG  
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTGTGCCCAGTGCACAAGTGGCCAG  
TTCTCACCCCTGCTCTGTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA  
CTGTCATCTCCTGGTTCTGCTCTTTATTGGTGAATCTGGTCTCTGGCTTCTTCGGCGTTCACT  
CATTGTGTGCACCTCAGCTGAAAGTCTGCTACTCTGTGGCTCTGTCAGGCTGGCAGGCT  
GCCCTTCGTTACCAAGACTCTGTTGAACACCTGGTGTGTCAGTGGCAGTGCCTGGAC  
AGGGGCCCTCAGGGAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGTGTCCGACACAGGTG  
TTCACATCTGTGCTGTCAGGTCAAGTGCCTCAGTTCTGGAAGCTAGGTCTCGCAGTGTAC  
CAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAGGCCAGCTGAGGGGGTGTGAA  
TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCACTGAGCTGAGGAAGAGACAATCGGCCAG  
CACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACACTCATCTGCCACCCAGAATGCATCCT  
GCCTCATCAGGTCCAGATTCTTCCAAGGGCGACGTTCTGGAATTCTAGTCCTGGCC  
TCGGACACCTTCTTCGTTAGCTGGGAGTGGTGGTGAAGGCACTGAAGAAGAGGGGATGGTCAC  
ACTCAGATCCACAGAGGCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGCCCC  
ACCCCAACCCCTGCACGCCCTCATCCCCCTTGGCTTGAAGCCAGGCTGAGGCCAGGATGATCTGT  
CTGACCGAGACACTCACAGCTTGTCAAGGCACAGGCTCTCGGAGGCCAGGATGATCTGT  
CCACGCTTGCACCTCGGGCCCATCTGGCTCATGCTCTCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFVSDYTEVDNNV  
TRHLDKVLKRGDWDLILHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLLISSAFERKPGDIRHPKHQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## **FIGURE 141**

GGCACGAGGAAGCCTTCCAGGTATCGTACGCACCTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAACAGCTGGCGTGGCACTGATGTTACTGCTGCTGGAGTACA  
TCCCTATAGAAAACA  
CTGCCAGCACCTTAAGACC  
ACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATT  
CAGCATT  
CATGACCAGGATCACAAAGTACTGGTCTGGACTCTGGGAA  
CTCTCAT  
AGCAGTTCCAGATA  
AAA  
ACTACATACGCCAGAGATCTT  
TGCA  
TTAGCCTCATCCTTGAGCT  
CAGCCTCTCGGGAGAAAGGAAGTCCGATTCTCTGGGGTCTCTAAAGGGGAGTTTGCTCTAC  
TGTGACAAGGATA  
AAAGGACAAAGT  
CATCC  
ATCC  
TCAGCTGAAGAAGGAGAA  
ACTGATGAAGCT  
GGCTGCCAAAAGGAATCAGCACGCCGGCC  
CTCATCTTT  
TAGGGCTCAGGTGGGCTCCTGG  
ACATGCTGGAGTCGGCGCTCACCCGGATGGT  
CATCTGCACCT  
CCTGC  
AATTGTAATGAGCCT  
GTTGGGGT  
GACAGATA  
AATTG  
GAGAACAGGAA  
ACATTG  
AATTTC  
ATTCAACCAGTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCC  
CATTGAACGCC  
TTCC  
TCGCT  
CACT  
ATT  
TTG  
AACT  
ATTG  
TATA  
AAA  
ACCCA  
AACCT  
GCT  
CACT

## **FIGURE 142**

MLLLLLEYNFPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGWSNMLESAHPGWFIGTSCNCNEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

### **FIGURE 143**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTAA  
TCCAGGATCCTGTCCCTGCTCTGTAGGAGTGCCTGTCAGTGTGGGTGAGACAAGTTG  
TCCCACAGGGCTGCTGAGCAGATAAGATTAAGGGCTGGGTCTGCTCAATTAACTCCTGTGGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCAACAGTCAGCACCATGCTGGCCTGCCGTGG  
AAGGGAGGTCTGCTCTGGCGCTGCTGCTCTTAGGCTCCAGATCCTGCTGATCTATGC  
CTGGCATTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGTCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTGAATTCTGGAAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTGAAGAGCAGACATTGACAACACTGCCATTCCAAGAAAGCACAG  
AGCTGAACAAACTTACCTGCTTCAACCATCAGCACCAGGCCCTGGATGACTCAGTCAGC  
CTCCTGAACAAAGACCTGCTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTGTCCATGT  
GCTGCTCCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTGTTGATCCTATTGATGTGTTGAGATCTCAGATCAGTGTGTTAGAAAATCC  
ACACATCTGAGCTAATCATGTAGTGTAGATCATTAAACATCAGCATTAAAGAAAAAAAAAAAAA  
AAA

## **FIGURE 144**

MLGLPWKGGLSWALLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTCGAGGGCTCCAGAGGCACACTCCAGAGAGGCCAAGGTTCTGACCGGATGAGGAAG  
CACCTGAGCTGGTGGCTGGCACTGTGATGCTGCTTCAGCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGGCCAGGTGGCTGAGAACCGCCGGAGCCTCATCAAGCAAGGCCGCAAGCTGACATT  
GACTTCGGAGCCAGGGCAACAGGTACTACGAGGCCACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTTGAGGCTAATGTGACCAAGGAGGCATTGTACCGGCTGCATCAATGCCA  
CCCAGGCCGGAACCAGGGGGAGTTCCAGAAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTGGAGAGGGCGCAGGACT  
TCGGGTCAACCATGCACCAGCCAGTGCCTCTGCCTTGGCTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCAGGAGGCTGGCAGTACAGAGGCCAGCGAGCAAATCCTGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCATGCACTCGCACTGCAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCCTGATAAGATGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTCACAGTACTTCCAACAACTCTAGAGGTAG  
GTGTATTCCCCTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGCTTGTCTAACCCAGGTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGTACTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAAATGAAATTGTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNLHQQ  
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWLVMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCAAAGGGCTGGGATTATAGCGTGACCAACATGTCAGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTCTGGCCTCCTCT  
CTGTCTCTTCCCTCTTCTTATTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTTGTCACTGGGGTAGGTCACTGAGTCTTAGTTTATTGGAAATTT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

## **FIGURE 149**

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCCTACCTGGAGACTGAC  
TCCC CGCGCCCCAACCCCTGTTATCCCTGACCGTCAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCGCCACACCCACCCCTCTGGCTCTTCTGTTTACTCCTCTTCAATTATA  
ACAAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGCCGAGCGTGGAAAGAATGGGTT  
CCTCGGGACCGGCACCTGGATTCTGGTGTAGTGCCTCCGATTCAAGCTTCCCAAACCTGGAGGAA  
GCCAAGACAAATCTACATAATAGAGAATTAGTGAGAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAACATATCCTCCAGAAAACAAGCCAGGTAGAGCAACTATTCTT  
TGTTGATAACTTGAACCTGCTAAAGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAGATGTTGATTCAACCAAGAATCGAAAATG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTCA  
TCAACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGTGCAGGATTATGAAG  
AAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGTTTACAAAATTAACTCAAAAGGAAGCCAAACAA  
TTATGAGGAGGATCCAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTGCTAAGGGAGAAAAGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTGGAAAGGAGAACTAAAACCTACAGTGAAGACAACTTGAGGAACCTCA  
ATATTCCCAAATTCTATGCGCTACTGAAAAGTATTGATTCAAGAAAAGAAGCAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTGTGAAGATGATGGTGAATATGGAACAATATCT  
CCAGAAGAAGGTGTTCTACCTTGAAACTGGATGAAATGATTGCTCTTCAGACCAAAACAAGCT  
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTCCAGCACCCTAGAGAAGATCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAGGAATATGGAAGCTGAAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTATTGGAAGC  
CATCAGAAAAAATATTGAATGGTGAAGAAACATGACAAAAGGAAATAAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTAGCAGCCTGTAAAATGGCAAAGATCCAGGAGTCTTCAA  
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCAATTCTGTGATTAAAATTGGACCCAAGG  
GTTATTAGAAAGTGTGAATTACAGTAGTTAACCTTACAAGTGGTTAAAACATAGCTTCTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMMAIQDGIAKGENETVSNTLTNTGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGTEAYLEAIRKNIEWLKKHDKGKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCAGGGCTCCGCCAGGAGAAAGAACATTCTGAGGGGAGTCTACACCCGTGGAGCTCAA  
GATGGTCCTGAGTGGGGCGCTGCTTCCGATGAAGGACTCGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGCTGATCGAGGAAGGTCAATTAAAGGTGAAGAGATCAGC  
GTGGTCCCCATCGTGGCTGGCATGCGAGCTGTCAGGGCTCATCCTGGGTGTCAGGGTGAAG  
CCAGTGGCTGTCATGTGGGTGGCAGGAGCAGCTAACAAGTAGAGCCAGTGAACATCATGG  
AGCTCTATCTGGTGCAGGAACTCAAGAGCTCACCTCTACCCGGGGACATGGGCTCACC  
TCCAGCTTGCAGTCGGCTGCCTACCCGGGTGGTCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCACTACCCAGCTCCCAGAATGGTGGCTGGAAATGCCCATCACAGACTTCACTTCC  
AGCAGTGTGACTAGGGCAACGTGCCCCAGAACCTCCGGCAGAGCCAGCTGGTGAGGGT  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCACTTGTCTCTGGTCCCCAGTTGGATAAAATTCTGAGATTGGAGCTCAGT  
CCACGGCTCTCCCCACTGGATGGTGCCTACIGCTGTGAACTTGATAAAACCATGTGGGTAAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGTGGGGAGTGGTGGGAATCATTCTGCT  
TAATGGTAACGTACAAGTGTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTATA  
GGGTCACTAGCTCCACATGAAGTCTGCACTCAACACTGTGCAAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCAGGCCACCCCTCCCTTAATCCTGCCACTGTCATA  
TGCTACCTTCTATCTCTCCCTCATCATCTGTGTGGCATGAGGAGGTGGTGTGAGTGTGAGAA  
GAAATGGCTCAGCTCAGAAGATAAGTAGAGGTATGCTGATCCTCTTTAAAAACCCAA  
GATACAATCAAATCCCAGATGCTGGTCTTATTCCATGAAAAGTGTCTGACATATTGAGA  
AGACCTACTTACAAGTGGCATATAATTGCAATTATTAAATTAAGATACCTATTATATT  
TCTTTATAGAAAAAAGTCTGGAAGAGTTACTTCATTGTAGCAATGTCAAGGGTGGCAGTAT  
AGGTGATTTCTTTAATTCTGTTAATTATCTGTATTTCTAATTCTACAATGAAGATGA  
ATTCCCTGTATAAAATAAGAAAAGATAATTCTGAGGTAAAGCAGAGCACATCATCTGAA  
TTGTCCTCAGCCTCCACTTCCAGAGTAAATTCAAAATTGAATCGAGCTCTGCTCTGGTTGG  
TTGTAGTAGTGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGAGTTGT  
GTGGCTGGAATCTCTGGTAAGGAACCTAAAGAACAAAAATCATCTGGAATTCTTCTAGAAG  
GATCACAGCCCCCTGGGATTCCAAGCCATTGGATCCAGCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGCCCCCTCAAATTCAACATCCTCTGGAAATCTCAGCTGTGAGTTATTGGAGATAAG  
GTCTCTGAGATGTAGTTAGTTAAAGACAAGGTATGCTGGATGAAGGTAGACCTAAATTCAATAT  
GACTGGTTCTTGTATGAAAAGAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTGCAGGCCAAAGCTAAGAAAACCCAAGGATTGTGGCAACC  
ATCAGAAAGCTTGGAGAGGCAAAGAAGAATTCTCCCTAGAGGTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTGAGCTTCCAGCCTCTGAACGAAGAAAGATAAAATTCCGCTGTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTTAGGAAACTAATACAGCTGCTAAATGATCCCTGT  
CTCCTCGTGTTCATTCTGTTGCTCTGCCCCACATGTACCAAAGTTGTCTTGTGACCAA  
TAGAATATGGCAGAAGTGTGATGGCATGCCACTTCAAGAATTAGGTATAAAAGACACTGCACTTC  
TACTTGAGCCCTCTCTGCCCCACCGCCCCAATCTATCTGGCTCACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCATAAAGAGACCTACGTGGAAAAATGAAGTCTCCT  
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTT  
AAGTTGCTCAGTTGGCTAACCTGTTATGCAGCAATAGATAAAATATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEELSVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

### **FIGURE 153**

CTTCAGAACAGGTTCTCCTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTTTCTTATGGGGACCTGGCCACCAGCTGCCTCCTCTTTGG  
CCCTCTGGTACAGGGAGGAGCAGCTGCCCATCAGCTCCACTGCAGGCTTGACAAGTCAAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTCGTCTCATGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCTGAAGAAAGTGTGTTCCCTCAATCTGATAGGTT  
CAGCCTATATGCAGGAGGTGGTGCCTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGTCTCTGAGAAAT  
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAACAAAAGGAAGATGGGAAGCCAAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTCTAAGCATAGATATTATTGATAAACATTCAATTGTAACTGGTGTTC  
TATACACAGAAAACAATTATTTAAATAATTGTCTTTCCATAAAAAAGATTACTTCCAT  
TCCTTAGGGAAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTATATTTATAAA  
TGTATTATTATTATTATAAGACTGCATTATTTATATCATTATTAATATGGATTATTAT  
AGAAACATCATTGATATTGCTACTTGAGTGTAAAGGCTAATATTGATATTATGACAATAATTAT  
AGAGCTATAACATGTTATTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKVSSFLMGTLATSCLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNNTDVRILIGEKLFHGVMSERCYLMQVLNFTLEEVLFQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAAGTCAGTGCCCGACTTGTGACTGAGTGACTGCCAGCATGTACCAGGTCAAGTGCAGAGGGC  
TGCCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCAAGC  
TGCCAGGTTGGGCTGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTCCTACAGGTGGTTGCAT  
TCTTGGCAATGGTATGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGAGGTGGAGCACTGTGCTGTGCCCTCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCTGTAGGGCAGTGAAGATGGACCCCTAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCGT  
TGCCTGTGCCCGACTGCCCTACAGACAGGCTCCACATGGACCCCCGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCCTGGAGCGCAGGCTGTACCGTGTTCCTAGCTTGTGTGTGCGGGCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGCCCTTTGGAAACCTGGAGGCCAGGTGTACA  
ACCACTGCCATGAAGGGCAGGATGCCAGATGCTTGGCCCTGTGAAGTGCTGTGAGCAG  
CAGGATCCGGGACAGGATGGGGCTTGGGAAACCTGCACTCTGCACATTGAAAGAG  
CAGCTGCTGCTAGGGCCGCCGAAGCTGGTGTCTGCTATTTCTCTCAGGAAAGGTTTCAA  
GTTCTGCCCTTCTGGAGGCCACCACTCTGTCTCTCTTCCATCCCTGCTACCCCTG  
GCCCAAGCACAGGCACTTCTAGATATTCCCCCTTGCTGGAGAAGAAAGGCCCTGGTTTATT  
TGTTTGTACTCATCACTCAGTGACCATCTACTTGGTGCAATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGAAGCTGTTATTGAATGTATAGAGATTATCCAAATAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTYSHWPSCCPKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGTGTGCAGGAGCGCCGTACCCGAGAGCC  
GACC GTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAACCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGACTATTCA  
ATTTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGTTGTTGAAGGCCACCAA  
GATTTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCCTGGTGGTAAATGGACATTTCCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTCATTGGGCCATAATATTCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTCACCTCACCAAGGCTGCCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGGAAAGCCTGTGGGATCCGAACATCACTGCTTGTAAAGAAGAATGAGGAGACA  
GTAGAAAGTGAACCTCACAAACACTCCCCTGGAAACAGATACTGGCTCTTATCCAACACAGCAC  
TATCATGGGTTTCTCAGGTGTTGAGCCACACCAGAAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGAETGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTCCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTGTGCTCTGCCACAAACAGCGTCCCTTCCCT  
GGATAACAAACAAAAGCAAGCCGGAGGCTGGCTGCCTCTCCTGCTGTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGACAGAAAGGATCAAGAAGACTTCTT  
TCTTACCAACCACACTACTGCCCTTCAATTAGGTTCTTACCCATCTGAAATATGTTCCA  
TCACACAATTGTTACTTCACTGAATTCTCAAAACATTGCAGAAGTGAGGTGATCCTTGAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTGCCACTAAAAGAAGGCA  
GCAGACAAAGTCGCTTCCCTTTCAATTAGGTTCTTACCCATCTGAAATATGTTCCA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTCCCCCTGCCTTAACCTTCTGCA  
GTGATCTAAGAAGCCAGATTCTGACAAATACGTGGTGGTCTACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCCATGAAGGATGCCACTGCTT  
CTGTGCAGAACATTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNVS梧  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEGDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVYPSEICFHHTICYFTEFL  
QNHCRCSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCVPKYHLMKDATAFCAELLHVVKQQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

## **FIGURE 159**

AGCCACCAGCGAACATGACAGTGAAGACCTGCATGCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGAAAATCCCCAAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTGGGACCCCAACGGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPAMVKYLLSILGLAFLSEAARKIPKGHTFFQKPESCPPPGGSMKLDIGIINEN  
QRVSMSRNIESRSTSPWNYTWTWDPNRPSEVVQAQCRLGCINAQKEDISMNSVPPIQQETLVV  
RRKHQGCSVFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

## **FIGURE 161**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG  
ACAGAGAGTGACAAAATACCCAGCACAGCCCCCTCGCCCCCTCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC  
AGGGCCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTTGCTGTCC  
TGGCACTGGGCCGAAGCCCAGTGGTCTTCTCTGGAGAGGCTGTGGGCCCTAGGACGCTACC  
CACTGCTCTCCGGCCTCTCTGCCGCTCTGGACAGTGACATACTCTGCCCTGCCCTGGGACAT  
CGTGCCTGCTCCGGGCCCTGCTGGCCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTGGCGTGCATGGGACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGGTGAGGAGCCTAGGAA  
TGCCTCTCTCCAGGCCAAGTCGTGCTCTCTCCAGGCCTACCCACTGCCCCCTGCGTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTGTGCAAGTTGGTCAGTGTGGCTCTGGTATATGAC  
TGCTTCAGGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTTACTCAGCCAGGTACGAGAA  
GGAACATCAACCACACACAGCAGCTGCCCTGCCCTGGCTAACGTGTCAAGCAGATGGTACA  
ACGTGCATCTGGTCTGAATGTCTTGAGGAGCAGCACTCGGCCCTCCCTGTACTGGAATCAG  
GTCCAGGGCCCCCAAAACCCGGTGCACAAAAACCTGACTGGACCGCAGATATTACCTGAA  
CCACACAGACCTGGTCTCTGCTCTGTATTAGGTGTGGCCTCTGGAACCTGACTCCGTAGGA  
CGAACATCTGCCCTTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCCACTG  
CGACTGCTGCCCTGCAGAGCTGGCTGGACGCCAGCTGCTGCCCTGGCGCAGAGCGGCACT  
GTGCTGGCGGGCTCCGGTGGGACCCCTGCCAGCCACTGGTCCCACCGCTTCTGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTCCCATTGCTGAAAGGCCACCTAACCTCTGTGTTCAAGGTG  
AACAGCTGGAGAACGCTGCAGCTGCAAGGAGTGTGACTCCCTGGGCTGACTCCCTGGGCTCTAAAGA  
CGATGTGCTACTGGAGACAGGAGGCCAGGACAACAGATCCCTGTGCGCTTGGAACCCA  
GTGGCTGTAACCTCACTACCCAGCAAAGCCTCACGAGGGCAGCTGCCCTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTGCAAGCTATGGGACGATGACTTGGAGCGCTATGGGCTG  
CCCCATGGACAAATACATCCACAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCACTCTTGGCG  
CTGCGCTTCCCTCATCCTCTCTCAAAAAGGATCACCGAAAGGGTGGCTGAGGCTCTGGAA  
CAGGACGTCGCTGGGGCGGCCAGGGGCCGGCTCTGCTCTACTCAGCCGATGA  
CTCGGGTTTCAGGCCCTGGGGCGCCCTGGCTGGCCCTGTGGCTGGCCAGCTGCCGCTGCGCTGG  
CCGTAGACCTGTGGAGCGCTGTAACTGAGGCGCAAGGGGGCGTGGCTTGGTTACCGCCAG  
CGGCCAGACCCCTGCAAGGGGGCGCTGGCTGGCTGGCTGGCGCT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTGCGGCCAGGGGCCACGGCCGACAGACGCCCTCC  
GCCCTCGCTCAGCTGCGTGTGCCGACTTCTGCAAGGGGCCGGCGCAGCTACGTGGGG  
GCCTGCTTCAGGAGCTGCTCCACCCGGACGCCGTACCGCCCTTTCCGCAACCGTGCCGTCTT  
CACACTGCCCTCCAACTGCCAGACTTCTGGGGGCCCTGCAAGCAGCCCTGCCGCTTCCG  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCGGGCCCTCAAGCAGCCCTGGATAGCTACTTC  
CATCCCCCGGGGACTCCCGCCGGACGCCGGTGGGACCGGGGCGGACCTGGGGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTCTAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRIWDSIDLCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVGHWEEPEDEEKFGGAADSGVEEPRNASIQAQVVLFSQAYPTARCVLLEVQVPAALVQFGQSVGSVSYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTQSWLLDAPCSLPAEAALCWRAPIGGDPCQPLVPPLSWENVTVDKLEFPPLLKGHPNLCVQVNSSEKLQLQECWLADSLGPLKDVLLETRGPQDNRSILCALEPSGCTSPLSKASTRAARLGEYLLQDLQSQCQLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVLGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRTLQEGGVVLLFSPGAVALCSEWLQDGVSAGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTPVVFPLSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251, 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617, 692-697, 696-701, 700-705

## **FIGURE 163**

GGGAGGGCTGTGCCAGCCCCATGAGGACGCTGCTGACCATCTGACTGTGGGATCCCTGGCT  
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCAGCACGTGAAATTCCAGTCAGCAACTTGA  
AAACATCCTGACGTGGGACAGGGCCAGAGGGCACCCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGAGAAGAAGGGTGTCAAGGGATCACCCGAAGTCTGC  
AACCTGACGGTGGAGACGGCAACCTCACGGAGCTACTATGCCAGGTACCGCT  
GTCAGTGCGGGAGGCCGGTCAGCCAACAGATGACTGACAGGTTCACTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGATCTCAAAGTGAGATGATTCAAGATGATTGTCATCCTA  
CCCCCACGCCAACCGTGCAGGCATGGCACCGGCTAACCTGGAAGACATCTTCATGACCTG  
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGAAAGCAGAGAGA  
ATATGAGTTCTCGGCTGACCCCTGACACAGAGTCTGGCACCATCATGATTGCGTTCCA  
CCTGGGCCAGGGAGGTGCCCCCTACATGTGCCAGTGAAAGACACTGCCAGACGGACATGGACC  
TAACCTCTCCGGAGCCTCTGTTCTCATGGGCTCCTGTCAGTACTCTGCTACCTGAG  
CTACAGATATGTCAACCAAGCCCTGCACCTCCAACTCCCTGAAACGTCCAGCGAGTCTGACTT  
TCCAGCCGCTGCCCTCATCCAGGAGCACGTCTGATCCCTGTTGACCTCAGGGCCCCAGC  
AGTCTGGCCCAGCCTGCACTTCCAGATCAGGGTGTGGACCCAGGGAGGCCAGGAGC  
TCCACAGCGGCATAGCCTGTCGAGATCACCTACTTACGGCAGCCAGACATCTCATCCTCCAGC  
CCTCCAACGTGCCACCTCCCCAGATCTCTCCCCACTGTCCTATGCCCAAAACGCTGCCCTGAG  
GTCGGGCCCCATCCTATGACCTCAGGTGACCCCCGAAGCTCAATTCCATTCTACGCCCA  
GGCCATCTCTAAGGTCAGCCTCCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
CCTATGGGTATGCAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTCTAGTCTAA  
CACCTTAGGCTAAAGGTCAAGCTCAGAAAGAGCCACCAAGCTGGAAGCTGCAATTGAGG  
TTCTCTGCAGGAGGTGACCTCCCTGGCTATGGAGGAATCCAAGAAGCAAATATTGCA  
CCCTGGGATTGACAGACAGAACATCTACCCAAATGTGCTACACAGTGGGAGGAAGGGACA  
CCACAGTACCTAAAGGGCAGCTCCCCCTCTCTCAGTCCAGATCGAGGGCACCCATGTC  
CCTCCCTTGTCAACCTCCCTGGTCACTGGGCTCAGGCTGACAGTCCCTGGG  
TGCTGGAGTCCCTGTGTGCTCCAGGATGAAGCCAAGGCCCAGCCCTGAGACCTCAGACCTG  
GAGCAGCCCCACAGAAGTCTGGATTCCTTCAAGAGGCTGGCCCTGACTGTGCA  
**AGGGGAATGGGAAAGGCTGGTCTCTCCCTGTCCTACCCAGTGTCACTCCCTGGCTGTCA**  
ATCCCAGCCTGCCCATGCCACACTCTCGCATCTGGCCTCAGACGGGTGCCCTTGAGAGAAC  
AGAGGGAGTGGCATGAGGGGGAGCTGGGAGCAGCTGGAGGAAATGCAAGGGAAACTCCCAG  
CAAGGAGAAAATGACAGTGCAGGAGGAAATGCAAGGGAAACTCCCAGGCTCAGAGCCCCACCTC  
CTAACACCATGGATTCAAAGTGTCAAGGAAATTGCTCTCCTGGCCCTTGTCAATTGTT  
ACAATCTAGCTGACAGAGCATGAGGCCCTGCCTTCTGTCAATTGTTCAAAGGTGGGAGAGA  
GCCTGGAAAAAGAACAGGCTGGAAAAGAACCAAGAGAACAGAAGGGCTGGCAGAACCA  
ACTTCTGCAAGGCCAGGGCAGGGCAGCAGGACTCTAGGGAGGGTGTGGCCTGAGCTCA  
TTCCCAAGGCCAACTGCTGACGTTGACGATTCTAGCTTCAATTCTCTGTATAGAACAAAGC  
GAAATGCAAGGTCACCAGGGAGGGAGACACACAAGCCTTTCTGCAGGAGGTTCA  
ATCCTGAGAAATGGGGTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGTACAATAACAC  
TGTACTGATGTCACAACCTTCAAGCTCTGCTTGGGCTCAGGCCATCTGGCTCAAATTCCAGC  
CTCACCACTACAAGCTGTGTCACTCAAAATGAAATCAGTGCCAGAACCTCGGTTCC  
ATCTGTAATGTGGGGATCATAACACTCATGGAGTTGTGGTGAAGATGAAAGTCA  
TCTTAAAGTGTCTTAATAGTGTCTGTCACTGGCAGGCCAATAACGGTAGCTATTAAAAA  
AAAAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCCRITRKSCNLTVETGNLTEYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVT CIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFGAFLFSMGFLAVLCYLSYRYVTKPPAP  
PNSLNQQRVLTFQPLRFIQEHLVLI PVFDLSPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQI LSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPAGSCMLGGLSLQEVTS LAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLKQQLPLLSSVQIEGHPM SLPLQPPSGPC  
SPSDQGPSPWGLLESLVCPKDEAKSPAPETS DLEQPTELDSLFRGLALT VQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAGTCACCCGGGCCGCGGTGCCACAACATGG  
CTGGCGGCCGGGCTGCTCTGGCTGGCTGGCGCTCTGGTGGTCCCAG  
TCGGATCTCAGCACGGACGGCTTCTGGACCTCAAAGTGTGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTGAAGACTTCACGGGCCGTATTGTCGTTGTGAATTAA  
AAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGGGGATCCCTGAACCTGGCTGGA  
AGTGTGAACACAGTTGGATATTTCAAAAGATTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCGTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTAGGATCTTGGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAACGAGCTTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCTGTGCTGAGCCGAGGCATTAGAGCTGATTAGAGGATGGAGAACGGTCTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT  
CCTGCCTAACGCTCAGGGAGTGCAGTCTCGTTGGACACTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGAAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTCGTTGGCATAAAATCTAAGTTGTTTACAAAGATTGTTTTAGTA  
CTAAGCTGCCTTGGCAGTTGCATTTGAGCAAACAAAAATATTATTCCCTTAAGTA  
AAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGLDEECMMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSPVEESKKAAEVSQHREKSPEESRGRELDPVPEPEAFRADSEDGEGA  
FSESTEGLQQQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAAGAGGCCGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGCTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAACTTC  
AGTCCCCAAACCGCGACCCCTCGAAGTCTTGAACCTCCAGCCCCGACATCCACCGCGGGCACAGG  
CGCGGCAGGCGCAGGTCCCGCGAAGGCGATGCGCGCAGGGGGTCGGGCAGCTGGCTCGGGC  
GGCAGGGAGTAGGGCCCAGGGAGGCAGGGAGGCTGCATATTCAAGAGTCGGGCTGCGCCCTG  
GGCAGAGGCCGCCCCCTCGCTCACGCAACACCTGCTGCTGCCACCGCGCGCATGAGCCGCGTG  
TCTCGCTGCTGCTGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTCTGCCCGCGCTGGTCAGC  
GCCAAAAGGTGTGTTTGTGACTTCAAGCATCCCTGCTACAAAATGGCTACTTCCATGAAC  
GTCCAGCCGAGTGAAGCTTCAGGAGGCACGCCCTGGCTGTGAGAGTGAAGGAGGAGTCCTCCTCA  
GCCTTGAGAATGAAGCAGAACAGAACAGTTAATAGAGAGCATGTTGAAAACCTGACAAAACCGGG  
ACAGGGATTCTGATGGTGAATTCTGGATAGGGCTTGAGGAATGGAGATGGCAAAACATCTGG  
TGCCTGCCAGATCTCTACCAAGTGGCTGATGGAAGCAATTCCAGTACCGAAACTGGTACACAG  
ATGAACCTTCCTCGGAAGTGAAAAGTGTGATGATCACCAACCAACTGCCAATCCTGGC  
CTTGGGGTCCCTACCTTACCAAGTGGATGATGACAGGTGTAACATGAAGCACAATTATATTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCTGAGAAAAGCCTTATCTACAAATCAACCAG  
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCAATCTAATTATGTGTT  
ATACCAACAATACCCCTGCTCTACTGATACTGGTTGCTTTGGAACCTGTTGAGATGCT  
GCATAAAAGTAAAGGAAGAACAAAAACTAGTCACCCAGTCTACACTGTGGATTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAAACTCATTGACTTGGTCCAGAATTGTAATTCT  
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTGGATGGCTGAAATCACAAAGGATCTGC  
AAGATGAACTGTAAGCTCCCCCTGAGGCAAATATTAAAGTAATTGTTATGTTGCTATTATTC  
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTGCTAAAGGATGCACCCAA  
ACTTCAAACCTCAAGCAAATGAAATGGACAATGAGATAAAAGTTGTTATCAACACGTCGGAGTA  
TGTGTGTTAGAAGCAATTCTTTATTCTTCACCTTCATAAGTGTATCTAGTCAATGTAA  
TGTATATTGTTGAAATTACAGTGTGCAAAGTATTACCTTGCATAAGTGTGATAAAA  
ATGAACGTGTTCTAATATTATTATGGCATCTCATTTCATAACATGCTTTGATTAAAG  
AAACTTATTACTGTTGTCACTGAATTCAACACACACAAATATAGTACCATAGAAAAGTTGT  
TTCTCGAAATAATTCAATTCTCAGCTCTGCTTTGGTCAATGTCTAGGAAATCTTCAGA  
AATAAGAAGCTATTCTATTAAAGTGTGATAAAACCTCCCAAACATTTACTTAGAGGCAAGGAT  
TGTCTAATTCAATTGTGCAAGACATGTGCCTATAATTATTAGCTTAAATAAACAGATT  
TTGTAATAATGTAACCTGTTAATAGGTGCATAAACACTAATGCAATTGAAACAAAAGAAG  
TGACATACACAATATAATCATATGCTTCACACGTTGCCATATAATGAGAACAGCAGCTCTGA  
GGGTTCTGAAATCAATGTGGCCCTCTTGCCCCTAAACAAAGATGGTTGTTGGGGTTGGG  
ATTGACACTGGAGGCAGATAGTGCAAAGTTAGTCTAAGGTTCCCTAGCTGTATTAGCCTCTG  
ACTATATTAGTATACAAAGAGGTATGTGGTTGAGACCAGGTGAATAGTCACATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTAGGAAGGAAAGGAACATCGAAATCGTGTGAAAATGGGTTGG  
AACCCATCAGTGTGATCGCATATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTT  
CTGCTTATCTCTAGTTCTCAATGCTACGCCCTGTTCAAGAGAAAAGTTGTAAC  
CTGGTCTTCATATGTCCTGCTCCTTTAACCAAATAAAGAGTTCTGTTCTGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGFRRVSGQKVCADFKHPCYK MAYFHELSSRVS FQE ARLACESE  
GGVLLSLENEAEQKLIESMLQNLT KPGTG ISDGDFWIGLWRNGDGQTSGACPDLYQWS DGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNL IYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ  
STLWISKSTRKESGM EV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-  
145, 212-217